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(54) Title: PROTEIN C PRODUCTION IN TRANSGENIC ANIMALS			
(57) Abstract			
<p>Methods for producing protein C in transgenic non-human mammals are disclosed. The protein C is modified at the two-chain cleavage site between the light and heavy chains of protein C from Lys-Arg to R₁-R₂-R₃-R₄ where R₁ through R₄ are individually Arg or Lys. DNA segments encoding modified protein C are introduced into the germ line of a non-human mammal, and the mammal or its female progeny produces milk containing protein C expressed from the introduced DNA segments. The protein C expressed from the introduced DNA segments has anticoagulant activity when activated. Non-human mammalian embryos and transgenic non-human mammals carrying DNA segments encoding heterologous protein C are also disclosed.</p>			

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DESCRIPTION

5 Protein C Production in Transgenic Animals

BACKGROUND OF THE INVENTION

Protein C in its activated form plays an important role in regulating blood coagulation. The 10 activated protein C, a serine protease, inactivates coagulation Factors Va and VIIIa by limited proteolysis. The coagulation cascade initiated by tissue injury, for example, is prevented from proceeding in an unimpeded chain-reaction beyond the area of injury by activated 15 protein C.

Protein C is synthesized in the liver as a single chain precursor polypeptide which is subsequently processed to a light chain of about 155 amino acids ($M_r = 21,000$) and a heavy chain of 262 amino acids ($M_r = 40,000$). 20 The heavy and light chains circulate in the blood as a two-chain inactive protein, or zymogen, held together by a disulfide bond. When a 12 amino acid residue peptide is cleaved from the amino terminus of the heavy chain portion of the zymogen in a reaction mediated by thrombin, the 25 protein becomes activated. The N-terminal portion of the light chain contains nine γ -carboxyglutamic acid (Gla) residues that are required for the calcium-dependent membrane binding and activation of the molecule. Another blood protein, referred to as "protein S", is believed to 30 accelerate the protein C-catalyzed proteolysis of Factor Va.

Protein C has also been implicated in the action of tissue-type plasminogen activator (Kisiel et al., Behring Inst. Mitt. 71:29-42, 1983). Infusion of bovine 35 activated protein C (APC) into dogs results in increased plasminogen activator activity (Comp et al., J. Clin. Invest. 68:1221-1228, 1981). Other studies (Sakata et

al., Proc. Natl. Acad. Sci. USA **82**:1121-1125, 1985) have shown that addition of APC to cultured endothelial cells leads to a rapid, dose-dependent increase in fibrinolytic activity in the conditioned media, reflecting increases in 5 the activity of both urokinase-related and tissue-type plasminogen activators. APC treatment also results in a dose-dependent decrease in anti-activator activity. In addition, studies with monoclonal antibodies against endogenous APC (Snow et al., FASEB Abstracts, 1988) 10 implicate APC in maintaining patency of arteries during fibrinolysis and limiting the extent of tissue infarct.

Experimental evidence indicates that protein C may be clinically useful in the treatment of thrombosis. Several studies with baboon models of thrombosis have 15 indicated that activated protein C in low doses will be effective in prevention of fibrin deposition, platelet deposition and loss of circulation (Gruber et al., Hemostasis and Thrombosis **374a**: abstract 1512, 1988; Widrow et al., Fibrinolysis **2** suppl. 1: abstract 7, 1988; 20 Griffin et al., Thromb. Haemostasis **62**: abstract 1512, 1989).

In addition, exogenous activated protein C has been shown to prevent the coagulopathic and lethal effects of gram negative septicemia (Taylor et al., J. Clin. 25 Invest. **19**:918-925, 1987). Data obtained from studies with baboons suggest that activated protein C plays a natural role in protecting against septicemia.

Until recently, protein C was purified from clotting factor concentrates (Marlar et al., Blood 30 **59**:1067-1072, 1982) or from plasma (Kisiel, J. Clin. Invest. **64**:761-769, 1979) and activated *in vitro*. However, the possibility that the resulting product could be contaminated with such infectious agents as hepatitis virus, cytomegalovirus, or human immunodeficiency virus 35 (HIV) make the process unfavorable.

While expression of protein C through recombinant means has been theoretically possible as the

genes for both human and bovine protein C are known (Foster et al., Proc. Natl. Acad. Sci. USA 82:4673-4677, 1985; Foster et al., Proc. Natl. Acad. Sci. USA 81:4766-4770, 1984 and U.S. Patent 4,775,624), it has been met 5 with limited success. Expression of some vitamin K-dependent proteins, such as protein C in cultured cells, has not produced protein C that has been at both commercially valuable levels and biologically functional when activated (i.e. had anticoagulant activity (Grinnell 10 et al., in Bruley and Drohn, eds., Protein C and Related Anticoagulants:29-63, Gulf Publishing, Houston, TX and Grinnell et al., Bio/Technol. 5:1189-1192, 1987)). Transgenic expression of protein C has yielded somewhat 15 higher levels of expression, but the recombinant protein's anticoagulant activity has still remained low, with less than 50% of the material having biological activity (Velander et al., Proc. Natl. Acad. Sci. USA 89:12003-12007, 1992). Therefore, there remains a need for 20 producing protein C that is both expressed at high levels and has therapeutic value.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide methods for producing protein C in transgenic 25 animals. It is a further object to provide transgenic animals that express human protein C in a mammary gland.

Within one aspect, the present invention provides methods for producing protein C in a transgenic animal comprising (a) providing a DNA construct comprising 30 a first DNA segment encoding a secretion signal and a protein C propeptide operably linked to a second DNA segment encoding protein C, wherein the encoded protein C comprises a two-chain cleavage site modified from Lys-Arg to R₁-R₂-R₃-R₄, and wherein each of R₁-R₄ is individually 35 Lys or Arg, and wherein said first and second segments are operably linked to additional DNA segments required for expression of the protein C DNA in a lactating mammary

gland of a host female animal; (b) introducing said DNA construct into a fertilized egg of a non-human mammalian species; (c) inserting said egg into an oviduct or uterus of a female of said species to obtain offspring carrying
5 said DNA construct; (d) breeding said offspring to produce female progeny that express said first and second DNA segments and produce milk containing protein C encoded by said second segment, wherein said protein has anticoagulant activity upon activation; (e) collecting
10 milk from said female progeny; and (f) recovering the protein C from the milk. In one embodiment, R₁-R₂-R₃-R₄ is Arg-Arg-Lys-Arg (SEQ ID NO: 20). In another embodiment, the method further comprises the step of activating the protein C. In another embodiment, the non-
15 human mammalian species is selected from sheep, rabbits, cattle and goats. In another embodiment each of the first and second DNA segments comprises an intron. In another embodiment, the second DNA segment comprises a DNA sequence of nucleotides as shown in SEQ ID NO: 1 or SEQ ID
20 NO:3. In another embodiment, the additional DNA segments comprise a transcriptional promoter selected from the group consisting of casein, β -lactogloulin, α -lactoglobulin, α -lactalbumin and whey acidic protein gene promoters.

25 In another aspect, the present invention provides a transgenic non-human female mammal that produces recoverable amounts of human protein C in its milk, wherein at least 90% of the human protein C in the milk is two-chain protein C.

30 In another aspect, the present invention provides a process for producing a transgenic offspring of a mammal comprising the steps of (a) providing a DNA construct comprising a first DNA segment encoding a secretion signal and a protein C propeptide operably
35 linked to a second DNA segment encoding protein C, wherein the encoded protein C comprises a two-chain cleavage site modified from Lys-Arg to R₁-R₂-R₃-R₄, and wherein each of

R_1-R_4 is individually Lys or Arg, and wherein said first and second segments are operably linked to additional DNA segments required for expression of the protein C DNA in a lactating mammary gland of a host female animal; (b) 5 introducing said DNA construct into a fertilized egg of a non-human mammalian species; and (c) inserting said egg into an oviduct or uterus of a female of said species to obtain offspring carrying said DNA construct.

Within another aspect, the present invention 10 provides non-human mammals produced according to the process for producing a transgenic offspring of a mammal comprising the steps of (a) providing a DNA construct comprising a first DNA segment encoding a secretion signal and a protein C propeptide operably linked to a second DNA 15 segment encoding protein C, wherein the encoded protein C comprises a two-chain cleavage site modified from Lys-Arg to $R_1-R_2-R_3-R_4$, and wherein each of R_1-R_4 is individually Lys or Arg, and wherein said first and second segments are operably linked to additional DNA segments required for 20 expression of the protein C DNA in a lactating mammary gland of a host female animal; (b) introducing said DNA construct into a fertilized egg of a non-human mammalian species; and (c) inserting said egg into an oviduct or uterus of a female of said species to obtain offspring 25 carrying said DNA construct.

In another aspect, the present invention provides a non-human mammalian embryo containing in its nucleus a heterologous DNA segment encoding protein C, wherein the encoded protein C comprises a two-chain 30 cleavage site modified from Lys-Arg to $R_1-R_2-R_3-R_4$, and wherein each of R_1-R_4 is individually Lys or Arg.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 illustrates analysis of plasma-derived 35 and transgenic protein C run under non-reducing and reducing conditions. Lane 1 is plasma-derived protein C

and lane 2 is transgenic protein C from the milk of sheep 30851.

Figure 2 illustrates sequencing of protein C from sheep line 30851. The initial yields were 5 prosequence=9 pmol, light chain=563 pmol and heavy chain=565 pmol.

Figure 3 illustrates clotting activity of transgenic protein C compared to plasma-derived protein C.

10 DETAILED DESCRIPTION OF THE INVENTION

Prior to setting forth the invention in detail, it will be helpful to define certain terms used herein:

As used herein, the term "biologically active" is used to denote protein C that is characterized by its 15 anticoagulant and fibrinolytic properties. Protein C, when activated, inactivates factor Va and factor VIIIa in the presence of phospholipid and calcium. Activated protein C also enhances fibrinolysis, an effect believed to be mediated by the lowering of the levels of 20 plasminogen activator inhibitors. As stated previously, two-chain protein C is activated upon cleavage of a 12 amino acid peptide from the amino terminus of the heavy chain portion of the zymogen.

The term "egg" is used to denote an unfertilized 25 ovum, a fertilized ovum prior to fusion of the pronuclei or an early stage embryo (fertilized ovum with fused pronuclei).

A "female mammal that produces milk containing biologically active protein C" is one that, following 30 pregnancy and delivery, produces, during the lactation period, milk containing recoverable amounts of protein C that can be activated to be biologically active. Those skilled in the art will recognize that such animals will naturally produce milk, and therefore the protein C, 35 discontinuously.

The term "progeny" is used in its usual sense to include offspring and descendants.

The term "heterologous" is used to denote genetic material originating from a different species than that into which it has been introduced, or a protein produced from such genetic material.

5 Within the present invention, transgenic animal technology is employed to produce protein C within a mammary gland of a host female mammal. Expression in the mammary gland and subsequent secretion of the protein of interest into the milk overcomes many difficulties

10 encountered in isolating proteins from other sources. Milk is readily collected, available in large quantities, and well characterized biochemically. Furthermore, the major milk proteins are present in milk at high concentrations (from about 1 to 16 g/l).

15 From a commercial point of view, it is clearly preferable to use as the host a species that has a large milk yield. While smaller animals such as mice and rats can be used (and are preferred at the proof-of-concept stage), within the present invention it is preferred to

20 use livestock mammals including sheep and cattle. Sheep are particularly preferred due to such factors as the previous history of transgenesis in this species, milk yield, generation time, cost and the ready availability of equipment for collecting sheep milk. It is generally

25 desirable to select a breed of host animal that has been bred for dairy use, such as East Friesland sheep, or to introduce dairy stock by breeding of the transgenic line at a later date. In any event, animals of known, good health status should be used.

30 Cloned DNA sequences encoding human protein C have been described (Foster and Davie, Proc. Natl. Acad. Sci. USA 81:4766-4770, 1984; Foster et al., Proc. Natl. Acad. USA 82:4673-4677, 1985; and Bang et al., U.S. Patent 4,755,624, each incorporated herein by reference).

35 Complementary cDNAs encoding protein C can be obtained from libraries prepared from liver cells of various mammalian species according to standard laboratory

procedures. DNAs from other species, such as the protein C encoded by rats, pigs, sheep, cows and primates can be used and can be identified using probes from human cDNA.

In a preferred embodiment, human genomic DNAs 5 encoding protein C are used. The human protein C gene is composed of nine exons ranging in size from 25 to 885 nucleotides, and seven introns ranging in size from 92 to 2668 nucleotides (U.S. Patent 4,959,318, incorporated herein by reference). The first exon is non-coding and 10 referred to as exon 0. Exon I and a portion of exon II code for the 42 amino acid signal sequence and propeptide (i.e., pre-propeptide). The remaining portion of exon II, exon III, exon IV, exon V and a portion of exon VI code for the light chain of protein C. The remaining portion 15 of exon VI, exon VII and exon VIII code for the heavy chain of protein C. A representative human genomic DNA sequence and corresponding amino acid sequence are shown in SEQ ID NOS: 1 and 2, respectively. A representative human protein C cDNA sequence and corresponding amino acid 20 sequences are shown in SEQ ID NO: 3 and 4, respectively.

Those skilled in the art will recognize that naturally occurring allelic variants of these sequences will exist; that additional variants can be generated by amino acid substitution, deletion, or insertion; and that 25 such variants are useful within the present invention. In general, it is preferred that any engineered variants comprise only a limited number of amino acid substitutions, deletions, or insertions, and that any substitutions are conservative. Thus, it is preferred to 30 produce protein C polypeptides that are at least 90%, and more preferably at least 95% or more identical in sequence to the corresponding native protein.

Within the present invention, the proteolytic processing involved in the maturation of recombinant 35 protein C from single chain form to the two-chain form (i.e., cleaved between the light chain and the heavy chain) has been enhanced by modifying the amino acid

sequence around the two-chain cleavage site. In the normal situation, endoproteolytic cleavage of the precursor molecule at the Arg₁₅₇-Asp₁₅₈ bond and the removal of the dipeptide Lys₁₅₆-Arg₁₅₇ by a 5 carboxypeptidase activity generate the light and heavy chains of protein C prior to secretion. Expression of protein C with the native (Lys-Arg) two-chain cleavage site produces protein C that may contain up to 40% or more uncleaved, single-chain protein C (Grinnel et al., in 10 Protein C and Related Anticoagulants, eds., Bruley and Drohan, Gulf, Houston, pp. 29-63, 1990; Suttie, Thromb. Res. 44:129-134, 1986 and Yan et al., Trends Biochem. Sci. 14:264-268, 1989). The single-chain form of protein C may not be able to be activated. The cleavage site may be in 15 the form of the amino acid sequence R₁-R₂-R₃-R₄, wherein each of R₁ through R₄ is individually lysine (Lys) or arginine (Arg). Particularly preferred sequences include Arg-Arg-Lys-Arg (SEQ ID NO: 20) and Lys-Arg-Lys-Arg (SEQ ID NO: 21).

20 In a preferred embodiment, the present invention provides for recoverable amounts of human protein C in the milk of a non-human mammal, where at least 90%, preferably at least 95%, of the human protein C is two-chain protein C.

25 To obtain expression in the mammary gland, a transcription promoter from a milk protein gene is used. Milk protein genes include those genes encoding caseins, beta-lactoglobulin (BLG), α -lactalbumin, and whey acidic protein. The beta-lactoglobulin promoter is preferred.

30 In the case of the ovine beta-lactoglobulin gene, a region of at least the proximal 406 bp of 5' flanking sequence of the ovine BLG gene (contained within nucleotides 3844 to 4257 of SEQ ID NO: 5) will generally be used. Larger portions of the 5' flanking sequence, up to about 5 kb, 35 are preferred. A larger DNA segment encompassing the 5' flanking promoter region and the region encoding the 5' non-coding portion of the beta-lactoglobulin gene

(contained within nucleotides 1 to 4257 of SEQ ID NO: 5) is particularly preferred. See Whitelaw et al., Biochem J. **286**: 31-39, 1992. Similar fragments of promoter DNA from other species are also suitable.

5 Other regions of the beta-lactoglobulin gene may also be incorporated in constructs, as may genomic regions of the gene to be expressed. It is generally accepted in the art that constructs lacking introns, for example, express poorly in the transgenic lactating mammary gland
10 in comparison with those constructs that contain introns (see Brinster et al., Proc. Natl. Acad. Sci. USA **85**: 836-840, 1988; Palmiter et al., Proc. Natl. Acad. Sci. USA **88**: 478-482, 1991; Whitelaw et al., Transgenic Res. **1**: 3-13, 1991; WO 89/01343; WO 91/02318). In this regard, it is
15 generally preferred, where possible, to use genomic sequences containing all or some of the native introns of a gene encoding protein C. Within certain embodiments of the invention, the further inclusion of at least some introns from the beta-lactoglobulin gene is preferred.
20 One such region is a DNA segment which provides for intron splicing and RNA polyadenylation from the 3' non-coding region of the ovine beta-lactoglobulin gene. When substituted for the natural 3' non-coding sequences of a gene, this ovine beta-lactoglobulin segment can both
25 enhance and stabilize expression levels of the protein C.

For expression of protein C, DNA segments encoding protein C are operably linked to additional DNA segments required for their expression to produce expression units. One such additional segment is the
30 above-mentioned milk protein gene promoter. Sequences allowing for termination of transcription and polyadenylation of mRNA may also be incorporated. Such sequences are well known in the art, for example, one such termination sequence is the "upstream mouse sequence"
35 (McGeady et al., DNA **5**:289-298, 1986). The expression units will further include a DNA segment encoding a secretion signal operably linked to the segment encoding

the protein C polypeptide chain. The secretion signal may be a native protein C secretion signal or may be that of another protein, such as a milk protein. The term "secretion signal" is used herein to denote that portion 5 of a protein that directs it through the secretory pathway of a cell to the outside. Secretion signals are most commonly found at the amino termini of proteins. See, for example, von Heinje, Nuc. Acids Res. 14: 4683-4690, 1986; and Meade et al., U.S. Patent No. 4,873,316, which are 10 incorporated herein by reference.

Construction of expression units is conveniently carried out by inserting a protein C sequence into a plasmid or phage vector containing the additional DNA segments, although the expression unit may be constructed 15 by essentially any sequence of ligations. It is particularly convenient to provide a vector containing a DNA segment encoding a milk protein and to replace the coding sequence for the milk protein with that of a protein C (including a secretion signal), thereby creating 20 a gene fusion that includes the expression control sequences of the milk protein gene. In any event, cloning of the expression units in plasmids or other vectors facilitates the amplification of the protein C sequences. Amplification is conveniently carried out in bacterial 25 (e.g. *E. coli*) host cells, thus the vectors will typically include an origin of replication and a selectable marker functional in bacterial host cells.

The expression unit is then introduced into 30 fertilized eggs (including early-stage embryos) of the chosen host species. Introduction of heterologous DNA can be accomplished by one of several routes, including pronuclear microinjection (e.g. U.S. Patent No. 4,873,191), retroviral infection (Jaenisch, Science 240: 1468-1474, 1988) or site-directed integration using 35 embryonic stem (ES) cells (reviewed by Bradley et al., Bio/Technology 10: 534-539, 1992). The eggs are then implanted into the oviducts or uteri of pseudopregnant

females and allowed to develop to term. Offspring carrying the introduced DNA in their germ line can pass the DNA on to their progeny in the normal, Mendelian fashion, allowing the development of transgenic herds.

5 General procedures for producing transgenic animals are known in the art. See, for example, Hogan et al., Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory, 1986; Simons et al., Bio/Technology 6: 179-183, 1988; Wall et al., Biol.

10 Reprod. 32: 645-651, 1985; Buhler et al., Bio/Technology 8: 140-143, 1990; Ebert et al., Bio/Technology 9: 835-838, 1991; Krimpenfort et al., Bio/Technology 9: 844-847, 1991; Wall et al., J. Cell. Biochem. 49: 113-120, 1992; and WIPO publications WO 88/00239, WO 90/05188, WO 92/11757; and GB 15 87/00458, which are incorporated herein by reference.

Techniques for introducing foreign DNA sequences into mammals and their germ cells were originally developed in the mouse. See, e.g., Gordon et al., Proc. Natl. Acad. Sci. USA 77: 7380-7384, 1980; Gordon and Ruddle, Science 20 214: 1244-1246, 1981; Palmiter and Brinster, Cell 41: 343-345, 1985; Brinster et al., Proc. Natl. Acad. Sci. USA 82: 4438-4442, 1985; and Hogan et al. (ibid.). These techniques were subsequently adapted for use with larger animals, including livestock species (see e.g., WIPO 25 publications WO 88/00239, WO 90/05188, and WO 92/11757; and Simons et al., Bio/Technology 6: 179-183, 1988). To summarize, in the most efficient route used to date in the generation of transgenic mice or livestock, several hundred linear molecules of the DNA of interest are 30 injected into one of the pro-nuclei of a fertilized egg. Injection of DNA into the cytoplasm of a zygote can also be employed.

In general, female animals are superovulated by treatment with follicle stimulating hormone, then mated. 35 Fertilized eggs are collected, and the heterologous DNA is injected into the eggs using known methods. See, for example, U.S. Patent No. 4,873,191; Gordon et al., Proc.

Natl. Acad. Sci. USA 77: 7380-7384, 1980; Gordon and Ruddle, Science 214: 1244-1246, 1981; Palmiter and Brinster, Cell 41: 343-345, 1985; Brinster et al., Proc. Natl. Acad. Sci. USA 82: 4438-4442, 1985; Hogan et al., 5 Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory, 1986; Simons et al. Bio/Technology 6: 179-183, 1988; Wall et al., Biol. Reprod. 32: 645-651, 1985; Buhler et al., Bio/Technology 8: 140-143, 1990; Ebert et al., Bio/Technology 9: 835-838, 10 1991; Krimpenfort et al., Bio/Technology 9: 844-847, 1991; Wall et al., J. Cell. Biochem. 49: 113-120, 1992; WIPO publications WO 88/00239, WO 90/05118, and WO 92/11757; and GB 87/00458, which are incorporated herein by reference.

15 For injection into fertilized eggs, the expression units are removed from their respective vectors by digestion with appropriate restriction enzymes. For convenience, it is preferred to design the vectors so that the expression units are removed by cleavage with enzymes 20 that do not cut either within the expression units or elsewhere in the vectors. The expression units are recovered by conventional methods, such as electro-elution followed by phenol extraction and ethanol precipitation, sucrose density gradient centrifugation, or combinations 25 of these approaches.

30 DNA is injected into eggs essentially as described in Hogan et al., ibid. In a typical injection, eggs in a dish of an embryo culture medium are located using a stereo zoom microscope (x50 or x63 magnification preferred). Suitable media include Hepes (N-2-hydroxyethylpiperazine-N'-2-ethanesulphonic acid) or bicarbonate buffered media such as M2 or M16 (available from Sigma Chemical Co., St. Louis, USA) or synthetic oviduct medium (disclosed below). The eggs are secured 35 and transferred to the center of a glass slide on an injection rig using, for example, a drummond pipette complete with capillary tube. Viewing at lower (e.g. x4)

magnification is used at this stage. Using the holding pipette of the injection rig, the eggs are positioned centrally on the slide. Individual eggs are sequentially secured to the holding pipette for injection. For each 5 injection process, the holding pipette/egg is positioned in the center of the viewing field. The injection needle is then positioned directly below the egg. Preferably using x40 Nomarski objectives, both manipulator heights are adjusted to focus both the egg and the needle. The 10 pronuclei are located by rotating the egg and adjusting the holding pipette assembly as necessary. Once the pronucleus has been located, the height of the manipulator is altered to focus the pronuclear membrane. The injection needle is positioned below the egg such that the 15 needle tip is in a position below the center of the pronucleus. The position of the needle is then altered using the injection manipulator assembly to bring the needle and the pronucleus into the same focal plane. The needle is moved, via the joy stick on the injection 20 manipulator assembly, to a position to the right of the egg. With a short, continuous jabbing movement, the pronuclear membrane is pierced to leave the needle tip inside the pronucleus. Pressure is applied to the injection needle via, for example, a glass syringe until 25 the pronucleus swells to approximately twice its volume. At this point, the needle is slowly removed. Reverting to lower (e.g. x4) magnification, the injected egg is moved to a different area of the slide, and the process is repeated with another egg.

30 After the DNA is injected, the eggs may be cultured to allow the pronuclei to fuse, producing one-cell or later stage embryos. In general, the eggs are cultured at approximately the body temperature of the species used in a buffered medium containing balanced 35 salts and serum. Surviving embryos are then transferred to pseudopregnant recipient females, typically by inserting them into the oviduct or uterus, and allowed to

develop to term. During embryogenesis, some of the injected DNA integrates in a random fashion in the genomes of a small number of the developing embryos.

Potential transgenic offspring are screened via 5 blood samples and/or tissue biopsies. DNA is prepared from these samples and examined for the presence of the injected construct by techniques such as polymerase chain reaction (PCR; see Mullis, U.S. Patent No. 4,683,202) and Southern blotting (Southern, J. Mol. Biol. 98:503, 1975; 10 Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, 1982). Founder transgenic animals, or G0s, may be wholly transgenic, having transgenes in all of their cells, or mosaic, having transgenes in only a subset of cells (see, for example, 15 Wilkie et al., Develop. Biol. 118: 9-18, 1986). In the latter case, groups of germ cells may be wholly or partially transgenic. In the latter case, the number of transgenic progeny from a founder animal will be less than the expected 50% predicted from Mendelian principles. 20 Founder G0 animals are grown to sexual maturity and mated to obtain offspring, or G1s. The G1s are also examined for the presence of the transgene to demonstrate transmission from founder G0 animals. In the case of male G0s, these may be mated with several non-transgenic 25 females to generate many offspring. This increases the chances of observing transgene transmission. Female G0 founders may be mated naturally, artificially inseminated or superovulated to obtain many eggs which are transferred to surrogate mothers. The latter course gives the best 30 chance of observing transmission in animals having a limited number of young. The above-described breeding procedures are used to obtain animals that can pass the DNA on to subsequent generations of offspring in the normal, Mendelian fashion, allowing the development of, 35 for example, colonies (mice), flocks (sheep), or herds (pigs, goats and cattle) of transgenic animals.

The milk from lactating G0 and G1 females is examined for the expression of the heterologous protein using immunological techniques such as ELISA (see Harlow and Lane, Antibodies. A Laboratory Manual, Cold Spring Harbor Laboratory, 1988) and Western blotting (Towbin et al., Proc. Natl. Acad. Sci. USA 76: 4350-4354, 1979). For a variety of reasons known in the art, expression levels of the heterologous protein will be expected to differ between individuals.

A satisfactory family of animals should satisfy three criteria: they should be derived from the same founder G0 animal; they should exhibit stable transmission of the transgene; and they should exhibit acceptably stable expression levels from generation to generation and from lactation to lactation of individual animals. These principles have been demonstrated and discussed (Carver et al., Bio/Technology 11: 1263-1270, 1993). Animals from such a suitable family are referred to as a "line." Initially, male animals, G0 or G1, are used to derive a flock or herd of producer animals by natural or artificial insemination. In this way, many female animals containing the same transgene integration event can be quickly generated from which a supply of milk can be obtained.

The protein C is recovered from milk using standard practices such as skimming, precipitation, filtration and protein chromatography techniques.

Protein C produced according to the present invention can be activated by removal of the activation peptide from the amino terminus of the heavy chain. Activation can be achieved using methods that are well known in the art, for example, using α -thrombin (Marlar et al., Blood 59:1067-1072, 1982), trypsin (Marlar et al., 1982, ibid.), Russel's viper venom factor X activator (Kisiel, J. Clin. Invest. 64:761-769, 1979) or commercially available Protac C (American Diagnostics, NY, NY).

The protein C molecules provided by the present invention and pharmaceutical compositions thereof are particularly useful for administration to humans to treat a variety of conditions involving intravascular coagulation. For instance, although deep vein thrombosis and pulmonary embolism can be treated with conventional anticoagulants, the activated protein C described herein may be used to prevent the occurrence of thromboembolic complications in identified high risk patients, such as those undergoing surgery or those with congestive heart failure. Since activated protein C is more selective than heparin, being active in the body generally when and where thrombin is generated and fibrin thrombi are formed, activated protein C will be more effective and less likely to cause bleeding complications than heparin when used prophylactically for the prevention of deep vein thrombosis. The dose of activated protein C for prevention of deep vein thrombosis is in the range of about 100 µg to 100 mg/day, and administration should begin at least about 6 hours prior to surgery and continue at least until the patient becomes ambulatory. In established deep vein thrombosis and/or pulmonary embolism, the dose of activated protein C ranges from about 100 µg to 100 mg as a loading dose followed by maintenance doses ranging from 3 to 300 mg/day. Because of the lower likelihood of bleeding complications from activated protein C infusions, activated protein C can replace or lower the dose of heparin during or after surgery in conjunction with thrombectomies or embolectomies.

The activated protein C compositions of the present invention will also have substantial utility in the prevention of cardiogenic emboli and in the treatment of thrombotic strokes. Because of its low potential for causing bleeding complications and its selectivity, activated protein C can be given to stroke victims and may prevent the extension of the occluding arterial thrombus.

The amount of activated protein C administered will vary with each patient depending on the nature and severity of the stroke, but doses will generally be in the range of those suggested below.

5 Pharmaceutical compositions of activated protein C provided herein will be a useful treatment in acute myocardial infarction because of the ability of activated protein C to enhance *in vitro* fibrinolysis. Activated protein C can be given with tissue plasminogen activator
10 or streptokinase during the acute phases of the myocardial infarction. After the occluding coronary thrombus is dissolved, activated protein C can be given for subsequent days or weeks to prevent coronary reocclusion. In acute myocardial infarction, the patient is given a loading dose
15 of at least about 1-500 mg of activated protein C, followed by maintenance doses of 1-100 mg/day.

Activated protein C is useful in the treatment of disseminated intravascular coagulation (DIC). Patients with DIC characteristically have widespread
20 microcirculatory thrombi and often severe bleeding problems which result from consumption of essential clotting factors. Because of its selectivity, activated protein C will not aggravate the bleeding problems associated with DIC, as do conventional anticoagulants,
25 but will retard or inhibit the formation of additional microvascular fibrin deposits.

The invention is further illustrated by the following non-limiting examples.

30

EXAMPLES

Example IA. Vector pMAD6 Construction

35 The multiple cloning site of the vector pUC18 (Yanisch-Perron et al., *Gene* 33:103-119, 1985) was removed and replaced with a synthetic double stranded oligonucleotide (the strands of which are shown in SEQ ID

NO: 6 and SEQ ID NO: 7) containing the restriction sites Pvu I/Mlu I/Eco RV/Xba I/Pvu I/Mlu I, and flanked by 5' overhangs compatible with the restriction sites Eco RI and Hind III. pUC18 was cleaved with both Eco RI and Hind 5 III, the 5' terminal phosphate groups were removed with calf intestinal phosphatase, and the oligonucleotide was ligated into the vector backbone. The DNA sequence across the junction was confirmed by sequencing, and the new plasmid was called pUCPM.

10 The *b*-lactoglobulin (BLG) gene sequences from pSS1tgXS (disclosed in WIPO publication WO 88/00239) were excised as a Sal I-Xba I fragment and recloned into the vector pUCPM that had been cut with Sal I and Xba I to construct vector pUCXS. pUCXS is thus a pUC18 derivative 15 containing the entire BLG gene from the Sal I site to the Xba I site of phage SS1 (Ali and Clark, *J. Mol. Biol.* **199**: 415-426, 1988).

20 The plasmid pSS1tgSE (disclosed in WIPO publication WO 88/00239) contains a 1290 bp BLG fragment flanked by Sph I and EcoR I restriction sites, a region 25 spanning a unique Not I site and a single Pvu II site which lies in the 5' untranslated leader of the BLG mRNA. Into this Pvu II site was ligated a double stranded, 8 bp DNA linker (5'-GGATATCC-3') encoding the recognition site for the enzyme Eco RV. This plasmid was called pSS1tgSE/RV. DNA sequences bounded by Sph I and Not I restriction sites in pSS1tgSE/RV were excised by enzymatic 30 digestion and used to replace the equivalent fragment in pUCXS. The resulting plasmid was called pUCXSRV. The sequence of the BLG insert in pUCXSRV is shown in SEQ ID NO: 5, with the unique Eco RV site at nucleotide 4245 in the 5' untranslated leader region of the BLG gene. This site allows insertion of any additional DNA sequences under the control of the BLG promoter 3' to the 35 transcription initiation site.

Using the primers BLGAMP3 (5'-TGG ATC CCC TGC CGG TGC CTC TGG-3'; SEQ ID NO: 8) and BLGAMP4 (5'-AAC GCG

TCA TCC TCT GTG AGC CAG-3'; SEQ ID NO: 9) a PCR fragment of approximately 650 bp was produced from sequences immediately 3' to the stop codon of the BLG gene in pUCXSRV. The PCR fragment was engineered to have a BamH I site at its 5' end and an Mlu I site at its 3' end and was cloned as such into BamH I and Mlu I cut pGEM7zf(+) (Promega) to give pDAM200(+).

pUCXSRV was digested with Kpn I, and the largest, vector containing band was gel purified. This 10 band contained the entire pUC plasmid sequences and some 3' non-coding sequences from the BLG gene. Into this backbone was ligated the small Kpn I fragment from pDAM200(+) which, in the correct orientation, effectively engineered a Bam HI site at the extreme 5' end of the 2.6 15 Kbp of the BLG 3' flanking region. This plasmid was called pBLAC200. A 2.6 Kbp Cla I-Xba I fragment from pBLAC200 was ligated into Cla I-Xba I cut pSP72 vector (Promega), thus placing an Eco RV site immediately upstream of the BLG sequences. This plasmid was called 20 pBLAC210.

The 2.6 Kbp Eco RV-Xba I fragment from pBLAC210 was ligated into Eco RV-Xba I cut pUCXSRV to form pMAD6 (SEQ ID NO: 23). This, in effect, excised all coding and 25 intron sequences from pUCXSRV, forming a BLG minigene consisting of 4.2 Kbp of 5' promoter and 2.6 Kbp of 3' downstream sequences flanking a unique Eco RV site. An oligonucleotide linker (ZC6839: ACTACGTAGT; SEQ ID NO: 10) was inserted into the Eco RV site of pMAD6 (SEQ ID NO: 23). This modification destroyed the Eco RV site and 30 created a Sna BI site to be used for cloning purposes. The vector was designated pMAD6-Sna. Messenger RNA initiates upstream of the Sna BI site and terminates downstream of the Sna BI site. The precursor transcript will encode a single BLG-derived intron, intron 6, which 35 is entirely within the 3' untranslated region of the gene.

B. Intronless Vector pMAD

The beta-lactoglobulin cloning vector pMAD was also constructed to allow the insertion of cDNAs under the control of the beta-lactoglobulin gene promoter in constructs containing no introns. To generate pMAD, the plasmid pBLAC100 was opened by digestion with both Eco RV and Sal I. The vector fragment was gel purified and the linearized vector was ligated with the 4.2 kb promoter fragment from the plasmid pUCXSRV as a Sal I-Eco RV fragment. The resulting construct was designated pST1 and constitutes a beta-lactoglobulin mini-gene encompassing a 4.2 kb of promoter region and 2.1 kb of 3' non-coding region beginning immediately downstream of the beta-lactoglobulin translational termination codon. A unique Eco RV site allows blunt-end cloning of any additional DNA sequences. To generate transgenic animals it is generally accepted in the art and preferred to separate bacterial plasmid vector sequences from those intended to be used in the generation of transgenic animals. In order to allow the practical excision of novel cDNA based constructs using this beta-lactoglobulin mini-gene, the minigene was excised from pST1 on a Xho I-Not I fragment, the DNA termini made flush with Klenow polymerase and the product was ligated into the Eco RV site of pUCPM to yield pMAD. Digestion with Mlu I liberates beta-lactoglobulin-cDNA constructs from the bacterial vector backbone.

Intronless constructs based on cDNAs and vectors such as pMAD benefit from the use of "rescue technology" for efficient expression. Rescue technology takes advantage of the ability of a co-injected and co-integrated BLG gene to improve the expression levels obtained from intronless, cDNA-based constructs in the transgenic system. Rescue technology is disclosed in WIPO publication WO 92/11358, and is incorporated herein by reference.

Example 2A. Isolation of cDNA

A cDNA sequence coding for human protein C was prepared as described in U.S. Patent 4,959,318, which is incorporated herein by reference. Briefly, a genomic fragment containing an exon corresponding to amino acids -42 to -19 (SEQ ID NO: 1) of the pre-pro peptide of protein C was isolated, nick translated and used as a probe to screen a cDNA library constructed by the technique of Gubler and Hoffman, *Gene* 25:263-269, 1983, using mRNA from HepG2 cells. This cell line was derived from human hepatocytes and was previously shown to synthesize protein C (Fair and Bahnak, *Blood* 64:194-204, 1984). Positive clones comprising cDNA inserted into the Eco RI site of phage λ gt11 were isolated and screened with an oligonucleotide probe corresponding to the 5' non-coding region of the protein C gene. One clone was also positive with this probe and its entire nucleotide sequence was determined. The cDNA contained 70 bp of 5' untranslated sequence, the entire coding sequence for human preprotein C, and the entire 3' non-coding region corresponding to the second polyadenylation site.

B. Subcloning of Protein C cDNA

The vector pDX was derived from pD3, which was generated from plasmid pDHFRIII (Berkner et al., *Nuc. Acids Res.* 13:841-857, 1985). The Pst I site immediately upstream from the DHFR sequence in pDHFRIII was converted to a Bcl I site by digestion with Pst I. The DNA was phenol extracted, ethanol precipitated and resuspended in buffer B (50 mM Tris pH 8, 7 mM MgCl₂, 7 mM β -MSH). A ligation reaction containing the linearized plasmid DNA and Bcl I linkers was done. The resulting plasmid was phenol extracted, ethanol precipitated and digested with Bcl I and gel purified. The gel purified plasmid DNA was circularized by ligation and used to transform *E. coli* HB101. Positive colonies were identified by restriction

analysis and designated pDHFR'. DNA from positive colonies was isolated and used to transform dam⁻ E. coli.

Plasmid pD2' was generated by cleaving pDHFR' and pSV40 (comprising Bam HI digested SV40 DNA cloned into the Bam HI site of pML-1 (Lusky et al., Nature 291:79-81, 1981)) with Bcl I and Bam HI. The DNA fragments were resolved by gel electrophoresis, and the 4.9 kb pDHFR' fragment and 0.2 kb SV40 fragment were isolated. These fragments were used in a ligation reaction, and the resulting plasmid, designated pD2', was used to transform E. coli RRI.

Plasmid pD2' was modified by deleting the "poison" sequences in the pBR322 region (Lusky et al., 1981, ibid.). Plasmids pD2' and pML-1 were digested with Eco RI and Nru I. The 1.7 kb pD2' fragment and 1.8 kb pML-1 fragment were isolated by gel purification, circularized in a ligation reaction and used to transform E. coli HB101. Positive colonies were identified using restriction analysis (designated pD2) and digested with Eco RI and Bcl I. A 2.8 kb fragment (fragment C) was isolated and gel purified.

To generate the remaining fragments used in constructing pD3, pDHFRIII was modified to convert the Sac II (Sst II) site into either a Hind III or Kpn I site. pDHFRIII was digested with Sst II and ligation reactions with either Hind III or Kpn I linkers were done. The resultant plasmids were digested with either Hind III or Kpn I and gel purified. The resultant plasmids were designated either pDHFRIII (Hind III) or pDHFRIII (Kpn I). A 700 bp KpnI-Bgl II fragment (fragment A) was purified from pDHFRIII (Hind III).

The SV40 enhancer sequence was inserted into pDHFRIII (Hind III) by first digesting SV40 DNA with Hind III, and DNA from 5089 to 968 bp was isolated and purified. Plasmid pDHFRIII (Hind III) was phosphatased, and the SV40 DNA and linearized plasmid pDHFRIII (Hind III) were used in a ligation reaction. A 700 bp Eco RI-

Kpn I fragment (fragment B) was isolated from the resulting plasmid.

For the final construction of pD3, fragments A (50 ng), B (50 ng) and C (10 ng) were combined in a 5 ligation reaction and used to transform E. coli RRI. Positive colonies were isolated and plasmid DNA was prepared.

Plasmid pD3 was modified to accept the insertion of the protein C sequence by converting the Bcl I 10 insertion site to an Eco RI site. First, the Eco RI site present in pD3 (the leftmost terminus in adenovirus 5 0-1) was converted to a Bam HI site via conventional linkering procedures. The resultant plasmid was transformed in E. coli HB101. Plasmid DNA was prepared, and positive clones 15 were identified by restriction analysis.

pD3' is a vector identical to pD3 except that the SV40 polyadenylation signal (i.e., the SV40 Bam HI (2533 bp) to Bcl I (2770 bp) fragment) is in the late orientation. Thus, pD3' contains a Bam HI site as the 20 site of gene insertion.

To generate pDX, the Eco RI site in pD3' was converted to a Bcl I site by Eco RI cleavage, incubation with SI nuclease and subsequent ligation with Bcl I linkers. DNA was prepared from a positively identified 25 colony, and a 1.9 kb Xho I-Pst I fragment containing the altered restriction site was prepared via gel purification. In a second modification, Bcl I-cleaved pD3 was ligated with Eco RI-Bcl I adapters in order to generate an Eco RI site as the position for inserting a 30 gene into the expression vector. Positive colonies were identified by restriction analysis. The resulting plasmid, designated pDX, has a unique Eco RI site for insertion of foreign genes.

The protein C cDNA was inserted into pDX as an 35 Eco RI fragment. Plasmids were screened by restriction analysis. A plasmid having the protein C insert in the correct orientation with respect to the promoter elements

and plasmid DNA was designated pDX/PC. Because the cDNA insert in pDX/PC contains a ATG codon in the 5' non-coding region, deletion mutagenesis was performed on the cDNA. Deletion of the three base pairs was performed according 5 to standard procedures or oligonucleotide-directed mutagenesis. The pDX-based vector containing the modified cDNA was designated p594.

C. Modification of the Protein C Processing Site

10 To enhance the processing of single-chain protein C to the two-chain form, two additional arginine residues were introduced immediately upstream of the Lys₁₅₆-Arg₁₅₇ cleavage site of the precursor protein, resulting in a cleavage site consisting of four basic 15 amino acids, Arg-Arg-Lys-Arg (SEQ ID NO: 20). The resultant mutant precursor of protein C was designated PC962. It contains the sequence Ser-His-Leu-Arg-Arg-Lys-Arg-Asp (SEQ ID NO: 22) at the cleavage site. Processing at the Arg-Asp bond results in a two-chain protein C 20 molecule.

The mutant molecule was generated by altering the cloned cDNA by site-specific mutagenesis (essentially as described by Zoller and Smith, *DNA* 3:479-488, 1984, for the two-primer method) using the mutagenic oligonucleotide 25 ZC962 (5'AGTCACCTGAGAAGAAAACGAGACA^{3'}; SEQ ID NO: 11). Plasmid p594 was digested with Sst I, and the approximately 87 bp fragment was cloned into M13mp11 and single-stranded template DNA was isolated. Following mutagenesis, a correct clone was identified by sequencing. 30 Replicative form DNA was isolated, digested with Sst I, and the protein C fragment was inserted into Sst I-cut p594. Clones having the Sst I fragment inserted in the desired orientation were identified by restriction enzyme mapping. The resulting expression vector was designated 35 pDX/PC962.

D. Intronless Protein C Construct

To facilitate the cloning of the protein C cDNA, PC962, into pMAD, the cDNA contained in pEX/PC962 was modified to incorporate Eco RV sites at the extremities of the protein C cDNA insert. A 769 bp Sst II-Pst I fragment encompassing the 3' end of PC962 was cloned between the Sst II and Pst I sites of pBluescript II SK® (Stratagene, La Jolla, CA). The fragment was excised with Sst II and Eco RV and purified. The 5' portion of PC962 was modified by PCR. The sense oligonucleotide primer for this reaction covered the 5' ATG region of the cDNA and provided an Eco RV site upstream of this in the product. The antisense oligonucleotide primer covered the Sst II site used to generate the Sst II-Eco RV fragment. The resulting PCR product was digested with Eco RV and Sst II and ligated with the Sst II-Eco RV 3' fragment and Eco RV digested pMAD. The resulting plasmid, designated pCORP9 effectively contained the PC962 cDNA flanked by Eco RV sites in an intronless fusion driven by the beta-lactoglobulin promoter.

E. Genomic Protein C DNA Construction

A genomic DNA construct containing exons I through VIII was made. See, U.S. Patent 4,959,318, which is incorporated herein by reference, for disclosure of the exon structure of the protein C gene. This genomic construct, designated GPC10-1, changed the sequence 16 base pairs upstream of the ATG from the native protein C sequence to the beta-lactoglobulin sequence and introduced mutations in the propeptide cleavage site located in exon 2, and the two-chain cleavage site located in exon 6, as described below.

The construct was assembled using four fragments designated A, B, C and D and encompassed the protein C gene sequence from the ATG to a Bam HI site in exon VIII, immediately upstream of the stop codon. The fragments were generated from a human genomic library in λ Charon 4A phage that was screened with a radiolabeled cDNA probe for

human protein C. The screening of the λ library produced three clones that together mapped the entire protein C gene (Foster et al., 1985, *ibid.*). These clones were designated PC λ 1, PC λ 6 and PC λ 8.

5 Fragment A was a Not I to Eco RI fragment that contained exons I and II of the genomic sequence and was 1698 bp. A subclone of PC λ 6 contained an Eco RI to Eco RI fragment and was designated pHCR4.4-1. Using pHCR4.4-1 as a template and oligonucleotides ZC6303 (SEQ ID NO: 12) and 10 ZC6337 (SEQ ID NO: 13), a DNA fragment was generated by polymerase chain reaction (PCR). Oligonucleotide ZC6303 changed the sequence 16 base pairs 5' to the ATG sequence from the native protein C sequence to the equivalent sequence from the beta-lactoglobulin gene and introduced a 15 Not I site. Oligonucleotide ZC6337 changed the propeptide cleavage site from Arg-Ile-Arg-Lys-Arg (SEQ ID NO: 24) to Gln-Arg-Arg-Lys-Arg (SEQ ID NO: 25). The resulting PCR-generated fragment was digested with Not I and Bss HII, and a 1402 base pair fragment was gel purified and 20 designated A1. A second fragment was prepared using a λ gt11 clone of PC λ 1 as a template with oligonucleotides ZC6306 (SEQ ID NO: 14) and ZC6338 (SEQ ID NO: 15) in a polymerase chain reaction. The resulting DNA fragment, designated A3, was digested with Bss HII and Eco RI and 25 gel purified, resulting in a 296 base pair fragment. Fragments A1 and A3 were ligated into the Bluescript II KS[®] phagemid vector (Stratagene, La Jolla, CA). The resulting plasmid, designated GPC 2-2, was digested with Not I and Eco RI, gel purified and the Not I-Eco RI DNA 30 fragment was designated Fragment A.

PCR 2-14 is a subclone that contains an Eco RI to Eco RI DNA fragment of PC λ 8 (Foster et al., 1985, *ibid.*). The plasmid was digested with Eco RI and Sst I and gel purified. The resulting fragment was designated 35 Fragment B.

Plasmid PCR 2-14 was used as template DNA with oligonucleotides ZC6373 (SEQ ID NO: 16) and ZC6305 (SEQ ID

NO: 17), which introduced an Afl II site and the RRKR mutation of the native (KR) two-chain cleavage site, in a polymerase chain reaction. The resulting PCR-generated fragment was digested with Bgl II and Afl II and gel 5 purified, resulting in a 1441 base pair fragment, designated E1. Fragment E1 was used in a ligation reaction with oligonucleotides ZC6302 (SEQ ID NO: 18) and ZC6304 (SEQ ID NO: 19). These oligonucleotides form Afl II and Sst II restriction sites when annealed and were 10 ligated to the 3' end of fragment E1, resulting in a fragment with a 5' Bgl II site and a 3' Sst II site. This fragment was used in a ligation reaction with a Bam HI-Sst II digested Bluescript II KS[®] phagemid vector (Stratagene). The resulting plasmid was designated GPC 8- 15 5 and digested with Sst I and Sst II, generating a 626 base pair fragment, designated Fragment C.

A fourth fragment was generated by digestion of a genomic subclone (pHCB7-1) of PC18. pHCB7-1 contained a Bgl II to Bgl II fragment that encompassed exons VI 20 through VIII. pHCB7-1 was digested with Sst II and Bam HI and a 2702 base pair fragment was gel purified. The fragment was designated Fragment D.

A five-part ligation reaction was prepared using Not I and Bam HI digested and linearized Bluescript II KS[®] 25 phagemid vector (Stratagene) with Fragment A (5' Not I to 3' Eco RI) that contained exons I and II, Fragment B (5' Eco RI to 3' Sst I) that contained exons III, IV and V, Fragment C (5' Sst I to 3' Sst II) that contained the 5' portion of exon VI and Fragment D (5' Sst II to 3' Bam HI) 30 that contained the remaining 3' portion of exon VI and exons VII and VIII. The resulting DNA was 8950 base pairs and designated GPC 10-1.

GPC10-1 was originally generated with BLG sequences and a Not I site upstream of the ATG initiator 35 codon and modifications to both cleavage sites. A clone, designated pPC12/BS, was generated to ensure that the 5' Not I site of GPC10-1 would not introduce secondary

structure into mRNA molecules that could hinder translation. pPC12/BS was generated using PCR amplification of a 1 kb Not I-Sca I fragment that covered the 5' region of the protein C gene and contained the 5 wild-type ATG codon environment. This introduced an Eco RV site immediately downstream of the Not I site, adjacent to the ATG codon, and a Bam HI site was incorporated 3' of the Sca I site to facilitate cloning. Following a Not I/Bam HI digestion, the PCR product was cloned into Not I-10 Bam HI, digested Bluescript II KS® phagemid vector (Stratagene). The Not I-Eco RV-Sca I fragment present in pPC12/BS was excised, purified and ligated to GPC10-1, which had been linearized with Not I and partially digested with Sca I (the pUC ampillicin gene has an 15 internal Sca I site). The resulting clone was designated GPC10-2 and possesses an Eco RV site immediately upstream of the ATG initiator codon.

GPC10-1 and GPC10-2 both terminated at the final Bam HI site in exon VIII of the protein C gene. To 20 reconstitute the 56 bp of sequence, ending at the termination codon, two oligonucleotides were synthesized with flanking Bam HI (5') and Bgl II (3') restriction sites. Following annealing of the oligonucleotides, the product was cloned into Bam HI digested pBST+ to generate 25 plasmid pPC3'. pBST+ is a derivative of pBS (Stratagene) with a new polylinker. The addition of the polylinker added Bgl II, Xho I, Nar I and Cla I restriction sites from the vector polylinker downstream of the destroyed Bgl II site of the oligonucleotide construct.

30 The Not I-Bam HI fragment of GPC10-1 was subcloned into Not I/Bam HI digested pPC3' to add 3' coding sequences of protein C, the TAG termination codon followed by Bgl II-Xho I-Nar I-Cla I. The 3' region of the protein C gene beginning with the Eco RV site in 35 intron V was excised from this plasmid on an Eco RV-Cla I fragment.

The Eco RV-Eco RV fragment from GPC10-2, covering the 5' portion of the protein C gene, and the above Eco RI-Cla I fragment covering the 3' portion of the protein C gene were combined between the Eco RV and Cla I sites of pMAD6 (SEQ ID NO: 23) to generate pCORP13. This effectively placed a genomic portion of the protein C gene with modified propeptide and two-chain cleavage sites under the control of the beta-lactoglobulin promoter.

A further genomic construct was generated from pCORP13 that contained only the modified two-chain cleavage site. This was achieved using PCR amplification to modify two fragments which resulting in restoration of the coding capability of exon 2 from the mutant Gln-Arg-Arg-Lys-Arg (SEQ ID NO: 25) to the wild-type Arg-Ile-Arg-Lys-Arg (SEQ ID NO: 24). pCORP13 was used as template for these reactions. The first fragment was 1.3 kb, which encompassed the 5' end of the protein C gene up to the Bam HI site in exon 2. For this reason, the sense primer was designed to add a Hind III site 5' to the Eco RV site proximal to the ATG initiation codon. The antisense primer was designed to restore the wild-type sequences in exon 2, which included a restored Bam HI site. A second fragment of 0.2 kb from the Bam HI site in exon 2 to the Xho I site in intron 2, was also amplified. The two fragments were combined in pGEMII (Promega, Madison, WI) to generate pGEMPC1.5. A 7.5 kb Xho I fragment from pCORP 13 was ligated to Xho I digested pGEMPC1.5 to generate a complete protein C genomic sequence covering exons 1-8 with a wild-type propeptide cleavage site and a modified two-chain cleavage site. The plasmid was designated pGEMPC14. The sequence was excised from pGEMPC14 as a Hind III/Sal I fragment. The DNA termini were repaired using a Klenow reaction and the fragment was blunt-end ligated into Eco RV digested pMAD6 (SEQ ID NO: 23) to generate pCORP14.

Example 3

Mice for initial breeding stocks (C57BL6J, CBACA) were obtained from Harlan Olac Ltd. (Bicester, UK). These were mated in pairs to produce F1 hybrid cross 5 (B6CBAF1) for recipient females, superovulated females, stud males and vasectomized males. All animals were kept on a 14 hour light/10 hour dark cycle and fed water and food (Special Diet Services RM3, Edinburgh, Scotland) ad libitum.

10 Transgenic mice were generated essentially as described in Hogan et al., Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory, 1986, which is incorporated herein by reference in its entirety. Female B6CBAF1 animals were superovulated at 4-5 weeks of 15 age by an i.p. injection of pregnant mares' serum gonadotrophin (FOLLIGON, Vet-Drug, Falkirk, Scotland) (5 iu) followed by an i.p. injection of human chorionic gonadotrophin (CHORULON, Vet-Drug, Falkirk, Scotland) (5 iu) 45 hours later. They were then mated with a stud male 20 overnight. Such females were next examined for copulation plugs. Those that had mated were sacrificed, and their eggs were collected for microinjection.

DNA was injected into the fertilized eggs as described in Hogan et al. (ibid.). Briefly, the vector 25 containing the protein C expression unit was digested with Mlu I, and the expression unit was isolated by sucrose gradient centrifugation. All chemicals used were reagent grade (Sigma Chemical Co., St. Louis, MO, U.S.A.), and all solutions were sterile and nuclease-free. Solutions of 30 20% and 40% sucrose in 1 M NaCl, 20 mM Tris pH 8.0, 5 mM EDTA were prepared using UHP water and filter sterilized. A 30% sucrose solution was prepared by mixing equal volumes of the 20% and 40% solutions. A gradient was prepared by layering 0.5 ml steps of the 40%, 30% and 20% 35 sucrose solutions into a 2 ml polyallomer tube and allowed to stand for one hour. 100 µl of DNA solution (max. 8 µg DNA) was loaded onto the top of the gradient, and the

gradient was centrifuged for 17-20 hours at 26,000 rpm, 15°C in a Beckman TL100 ultracentrifuge using a TLS-55 rotor (Beckman Instruments, Fullerton, CA, USA). Gradients were fractionated by puncturing the tube bottom 5 with a 20 ga. needle and collecting drops in a 96 well microtiter plate. 3 µl aliquots were analyzed on a 1% agarose mini-gel. Fractions containing the protein C DNA fragment were pooled and ethanol precipitated overnight at -20°C in 0.3M sodium acetate. DNA pellets were resuspended 10 in 50-100 µl UHP water and quantitated by fluorimetry. The protein C expression unit was diluted in Dulbecco's phosphate buffered saline without calcium and magnesium (containing, per liter, 0.2 g KCl, 0.2 g KH₂PO₄, 8.0 g NaCl, 1.15 g Na₂HPO₄) or in TE (10 mM Tris-HCl, 1 mM EDTA 15 pH 7.5). DNA concentration is adjusted to about 6 µg/ml, prior to injection into the eggs (~2 µl total DNA solution per egg).

Recipient females of 6-8 weeks of age are prepared by mating B6CBAF1 females in natural estrus with 20 vasectomized males. Females possessing copulation plugs are then kept for transfer of microinjected eggs.

Following birth of potential transgenic animals, tail biopsies are taken, under anesthesia, at four weeks of age. Tissue samples are placed in 2 ml of tail buffer 25 (0.3 M Na acetate, 50 mM NaCl, 1.5 mM MgCl₂, 10 mM Tris-HCl, pH 8.5, 0.5% NP40, 0.5% Tween 20) containing 200 µg/ml proteinase K (Boehringer Mannheim, Mannheim, Germany) and vortexed. The samples are shaken (250 rpm) at 55°-60°C for 3 hours to overnight. DNA prepared from 30 biopsy samples is examined for the presence of the injected constructs by PCR and Southern blotting. The digested tissue is vigorously vortexed, and 5 µl aliquots are placed in 0.5 ml microcentrifuge tubes. Positive and negative tail samples are included as controls. Forty µl 35 of silicone oil (BDH, Poole, UK) is added to each tube, and the tubes are briefly centrifuged. The tubes are incubated in the heating block of a thermal cycler (e.g.

Omni-gene, Hybaid, Teddington, UK) to 95°C for 10 minutes. Following this, each tube has a 45 μ l aliquot of PCR mix added such that the final composition of each reaction mix is: 50 mM KCl; 2 mM MgCl₂; 10 mM Tris-HCl (pH 8.3); 0.01% 5 gelatin; 0.1% NP40, 10% DMSO; 500 nM each primer, 200 μ M dNTPs; 0.02 U/ μ l Taq polymerase (Boehringer Mannheim, Mannheim, Germany). The tubes are then cycled through 30 repeated temperature changes as required by the particular primers used. The primers may be varied but in all cases 10 must target the BLG promoter region. This is specific for the injected DNA fragments because the mouse does not have a BLG gene. Twelve μ l of 5x loading buffer containing Orange G marker dye (0.25% Orange G (Sigma) 15% Ficoll type 400 (Pharmacia Biosystems Ltd., Milton Keynes, UK)) 15 is then added to each tube, and the reaction mixtures are electrophoresed on a 1.6% agarose gel containing ethidium bromide (Sigma) until the marker dye has migrated 2/3 of the length of the gel. The gel is visualized with a UV light source emitting a wavelength of 254 nm. Transgenic 20 mice having one or more of the injected DNA fragments are identified by this approach.

Positive tail samples are processed to obtain pure DNA. The DNA samples are screened by Southern blotting using a BLG promoter probe (nucleotides 2523-4253 25 of SEQ ID NO: 7).

Southern blot analysis of transgenic mice prepared essentially as described above demonstrated that approximately 10% of progeny contained protein C sequences. Examination of milk from positive animals by 30 reducing SDS polyacrylamide gel electrophoresis demonstrated the presence of protein C at concentrations up to 1 mg/ml.

Example 4

35 Donor ewes are treated with an intravaginal progesterone-impregnated sponge (CHRONOGEST Goat Sponge,

Intervet, Cambridge, UK) on day 0. Sponges are left in situ for ten or twelve days.

Superovulation is induced by treatment of donor ewes with a total of one unit of ovine follicle stimulating hormone (OFSH) (OVAGEN, Horizon Animal Reproduction Technology Pty. Ltd., New Zealand) administered in eight intramuscular injections of 0.125 units per injection starting at 5:00 pm on day -4 and ending at 8:00 am on day 0. Donors are injected 10 intramuscularly with 0.5 ml of a luteolytic agent (ESTRUMATE, Vet-Drug) on day -4 to cause regression of the corpus luteum, to allow return to estrus and ovulation. To synchronize ovulation, the donor animals are injected intramuscularly with 2 ml of a synthetic releasing hormone 15 analog (RECEPTAL, Vet-Drug) at 5:00 pm on day 0.

Donors are starved of food and water for at least 12 hours before artificial insemination (A.I.). The animals are artificially inseminated by intrauterine laparoscopy under sedation and local anesthesia on day 1. 20 Either xylazine (ROMPUN, Vet-Drug) at a dose rate of 0.05-0.1 ml per 10 kg bodyweight or ACP injection 10 mg/ml (Vet-Drug) at a dose rate of 0.1 ml per 10 kg bodyweight is injected intramuscularly approximately fifteen minutes before A.I. to provide sedation. A.I. is carried out 25 using freshly collected semen from a Poll Dorset ram. Semen is diluted with equal parts of filtered phosphate buffered saline, and 0.2 ml of the diluted semen is injected per uterine horn. Immediately pre- or post-A.I., donors are given an intramuscular injection of AMOXYPEN 30 (Vet-Drug).

Fertilized eggs are recovered on day 2 following starvation of donors of food and water from 5:00 pm on day 1. Recovery is carried out under general anesthesia induced by an intravenous injection of 5% thiopentone 35 sodium (INTRAVAL SODIUM, Vet-Drug) at a dose rate of 3 ml per 10 kg bodyweight. Anesthesia is maintained by inhalation of 1-2% Halothane/O₂/N₂O. To recover the

fertilized eggs, a laparotomy incision is made, and the uterus is exteriorized. The eggs are recovered by retrograde flushing of the oviducts with Ovum Culture Medium (Advanced Protein Products, Brierly Hill, West Midlands, UK) supplemented with bovine serum albumin of New Zealand origin. After flushing, the uterus is returned to the abdomen, and the incision is closed. Donors are allowed to recover post-operatively or are euthanized. Donors that are allowed to recover are given 10 an intramuscular injection of Amoxyphen L.A. at the manufacturer's recommended dose rate immediately pre- or post-operatively.

Plasmids containing the protein C DNA are digested with Mlu I, and the expression unit fragments are 15 recovered and purified on sucrose density gradients. The fragment concentrations are determined by fluorimetry and diluted in Dulbecco's phosphate buffered saline without calcium and magnesium or TE as described above. The concentration is adjusted to 6 lg/ml, and approximately 2 20 pl of the mixture is microinjected into one pronucleus of each fertilized eggs with visible pronuclei.

All fertilized eggs surviving pronuclear microinjection are cultured in vitro at 38.5°C in an atmosphere of 5% CO₂:5% O₂:90% N₂ and about 100% humidity 25 in a bicarbonate buffered synthetic oviduct medium (see Table) supplemented with 20% v/v vasectomized ram serum. The serum may be heat inactivated at 56°C for 30 minutes and stored frozen at -20°C prior to use. The fertilized eggs are cultured for a suitable period of time to allow 30 early embryo mortality (caused by the manipulation techniques) to occur. These dead or arrested embryos are discarded. Embryos having developed to 5 or 6 cell divisions are transferred to synchronized recipient ewes.

Table
Synthetic Oviduct Medium

5	<u>Stock A (Lasts 3 Months)</u>	
	NaCl	6.29 g
	KCl	0.534 g
	KH ₂ PO ₄	0.162 g
10	MgSO ₄ .7H ₂ O	0.182 g
	Penicillin	0.06 g
	Sodium Lactate 60% syrup	0.6 mls
	Super H ₂ O	99.4 mls
15	<u>Stock B (Lasts 2 weeks)</u>	
	NaHCO ₃	0.21 g
	Phenol red	0.001 g
	Super H ₂ O	10 mls
20	<u>Stock C (Lasts 2 weeks)</u>	
	Sodium Pyruvate	0.051 g
	Super H ₂ O	10 mls
25	<u>Stock D (Lasts 3 months)</u>	
	CaCl ₂ .2H ₂ O	0.262 g
	Super H ₂ O	10 mls
30	<u>Stock E (Lasts 3 months)</u>	
	Hepes	0.651 g
	Phenol red	0.001 g
	Super H ₂ O	10 mls
35	<u>To make up 10mls of Bicarbonate Buffered Medium</u>	
	STOCK A	1 ml
	STOCK B	1 ml
	STOCK C	0.07 ml
	STOCK D	0.1 ml
	Super H ₂ O	7.83 ml
40	Osmolarity should be 265-285 mOsm. Add 2.5 ml of heat inactivated sheep serum and filter sterilize.	
45	<u>To make up 10 mls of HEPES Buffered Medium</u>	
	STOCK A	1 ml
	STOCK B	0.2 ml
	STOCK C	0.07 ml
	STOCK D	0.1 ml
	STOCK E	0.8 ml
50	Super H ₂ O	7.83 ml

Table. cont.

5 Osmolarity should be 265-285 mOsm.
Add 2.5 ml of heat inactivated sheep serum
and filter sterilize.

10 Recipient ewes are treated with an intravaginal
progesterone-impregnated sponge (Chronogest Ewe Sponge or
Chronogest Ewe-Lamb Sponge, Intervet) left *in situ* for 10
or 12 days. The ewes are injected intramuscularly with
1.5 ml (300 iu) of a follicle stimulating hormone
substitute (P.M.S.G., Intervet) and with 0.5 ml of a
luteolytic agent (Estrumate, Coopers Pitman-Moore) at
15 sponge removal on day -1. The ewes are tested for estrus
with a vasectomized ram between 8:00 am and 5:00 pm on
days 0 and 1.

20 Embryos surviving *in vitro* culture are returned
to recipients (starved from 5:00 pm on day 5 or 6) on day
6 or 7. Embryo transfer is carried out under general
anesthesia as described above. The uterus is exteriorized
via a laparotomy incision with or without laparoscopy.
Embryos are returned to one or both uterine horns only in
ewes with at least one suitable corpora lutea. After
25 replacement of the uterus, the abdomen is closed, and the
recipients are allowed to recover. The animals are given
an intramuscular injection of Amoxypen L.A. at the
manufacturer's recommended dose rate immediately pre- or
post-operatively.

30 Lambs are identified by ear tags and left with
their dams for rearing. Ewes and lambs are either housed
and fed complete diet concentrates and other supplements
and or ad lib. hay, or are let out to grass.

35 Within the first week of life (or as soon
thereafter as possible without prejudicing health), each
lamb is tested for the presence of the heterologous DNA by
two sampling procedures. Following tail biopsy, within a
week, a 10 ml blood sample is taken from the jugular vein
into an EDTA vacutainer. Tissue samples are taken by tail

biopsy as soon as possible after the tail has become desensitized after the application of a rubber elastrator ring to its proximal third (usually within 200 minutes after "tailing"). The tissue is placed immediately in a 5 solution of tail buffer. Tail samples are kept at room temperature and analyzed on the day of collection. All lambs are given an intramuscular injection of Amoxypen L.A. at the manufacturer's recommended dose rate immediately post-biopsy, and the cut end of the tail is 10 sprayed with an antibiotic spray.

DNA is extracted from sheep blood by first separating white blood cells. A 10 ml sample of blood is diluted in 20 ml of Hank's buffered saline (HES; obtained from Sigma Chemical Co.). Ten ml of the diluted blood is 15 layered over 5 ml of Histopaque (Sigma) in each of two 15 ml screw-capped tubes. The tubes are centrifuged at 3000 rpm (2000 x g max.), low brake for 15 minutes at room temperature. White cell interfaces are removed to a clean 15 ml tube and diluted to 15 ml in HBS. The diluted cells 20 are spun at 3000 rpm for 10 minutes at room temperature, and the cell pellet is recovered and resuspended in 2-5 ml of tail buffer.

To extract DNA from the white cells, 10% SDS is added to the resuspended cells to a final concentration of 25 1%, and the tube is inverted to mix the solution. One mg of fresh proteinase K solution is added, and the mixture is incubated overnight at 45°C. DNA is extracted using an equal volume of phenol/chloroform (x3) and chloroform/isoamyl alcohol (x1). The DNA is then 30 precipitated by adding 0.1 volume of 3 M NaOAc and 2 volumes of ethanol, and the tube is inverted to mix. The precipitated DNA is spooled out using a clean glass rod with a sealed end. The spool is washed in 70% ethanol, and the DNA is allowed to partially dry, then is 35 redissolved in TE (10 mM Tris-HCl, 1 mM EDTA, pH 7.5).

DNA samples from blood and tail are analyzed by Southern blotting using probes for the BLG promoter region and the protein C coding regions.

5 Example 5

A founder female animal, designated 30851, which is transgenic for both BLG and pCOPR9 was generated. She has given rise to two sons and a transgenic daughter, designated 40387. Recombinant transgenic protein C was 10 purified from milk (from 30851) by a single chromatography step using a calcium-dependent monoclonal antibody affinity column. Briefly, the milk samples were pooled up to a volume of 40 ml. Two volumes of ice-cold 1 X TBS (50 mM Tris-HCl, 150 mM NaCl pH 6.5) and 200 mM EDTA, pH 6.5 15 were added to solubilise the caseins. The EDTA-treated milk solution was centrifuged at 15,000 rpm for 30 minutes at 4°C in a JA20 rotor (Beckman Instruments, Irvine, CA). After centrifugation, the upper lipid phase and the small pellet were discarded.

20 The EDTA-treated milk was diluted with an equal volume of ice-cold 1 X TBS and 133 mM CaCl₂ while stirring. A cloudy precipitate formed upon addition of the CaCl₂. The pH was quickly adjusted by addition of a few drops of 4 M NaOH, and the precipitate was 25 redissolved. Any remaining insoluble material was removed by filtration through a 0.45 µm filter.

The optical density of the solubilised milk was measured at 280 nm, and the protein concentration was calculated. The milk was diluted to a protein 30 concentration of 10 mg/ml using 1 X TBS containing CaCl₂ to give a final Ca⁺⁺ concentration of 25 mM. The milk was used to resuspend antibody-Sepharose that carried the immobilized Ca⁺⁺-dependent monoclonal antibody PCL-2, and had been washed in 1 X TBS and 25 mM CaCl₂. PCL-2 is a 35 monoclonal antibody that binds single chain and two chain protein C, whether or not they are gamma-carboxylated. The milk-Sepharose mixture was incubated overnight at 4°C.

The matrix was washed twice in batch with 1 x TBS and 25 mM CaCl₂ and packed into a glass column. The resin was washed at a flow rate of 1 ml/min with a calcium containing buffer and a stable baseline was achieved 5 before the bound protein was eluted with an isocratic elution using 1 X TBS and 25 mM EDTA, pH 6.5. Fractions containing protein C were pooled and concentrated to approximately 1 ml using an Amicon ultrafiltration unit with a 10 kDa cut-off membrane (Amicon, Danvers, MA).

10 The monoclonal antibody, PCL-2, was coupled to the activated Sepharose 4B as follows: 1 g (3.5 ml of gel) of cyanogen bromide activated Sepharose 4B (Pharmacia LKB Biotechnology, Piscataway, NJ) was swollen for 15 minutes in 1 mM HCl. The swollen gel was resuspended in 0.1 M 15 NaHCO₃, 0.5 M NaCl pH 8.3 and washed several times. The washed gel was resuspended in 11 ml of monoclonal antibody solution (PCL-2, 3.5 mg/ml in bicarbonate buffer pH 8.3) with a coupling ratio of approximately 10 mg/ml gel. Coupling was allowed to proceed for 2 h at room 20 temperature on a rotary mixer, and the gel was recovered by gentle centrifugation. The monoclonal supernatant was removed and replaced by 1 M ethanolamine in order to block any remaining sites on the Sepharose. Blocking was performed overnight at 4°C. Excess adsorbed protein was 25 removed by sequential acid and alkali washes (0.1 M acetate, 0.5 M NaCl pH 4.0; 0.1 M NaHCO₃, 0.5 M NaCl pH 8.3), and the coupled gel was stored in 50 mM Tris-HCl, 150 mM NaCl pH 6.5, 0.02% azide.

30 Example 6

Samples of purified recombinant transgenic protein C were compared with plasma-derived protein C and a plasma-derived activated protein C (APC) preparations. Samples were run on SDS PAGE 4-20% acrylamide gradient 35 gels under reducing conditions and silver stained for protein.

The plasma-derived material shows the presence of a heavy-chain doublet around 44 kDa (Figure 1, Lane 1). This has been reported to be due to partial occupancy of the three possible N-linked glycosylation sites on the 5 molecule. A similar doublet, although of a slightly lower mass presumably due to some subtle change in glycosylation profile, has also been seen with the transgenic protein C. The light chain was visible around 22 kDa for both preparations. Significantly, in the case of the plasma-10 derived material uncleaved single-chain was clearly visible above the heavy chain doublet. Plasma-derived protein normally contained 5-10 percent of this inactive material. In contrast, the transgenic protein C contains no obvious single chain by this gel analysis. Therefore, 15 it contains less than a few percent at most of inactive material. This most likely reflects the increased efficiency of cleavage of the modified inter-chain site. In further support of this observation no single chain was visible by direct western blot analysis of transgenic 20 sheep milk (40387, expression level 300 µg/ml).

The purified transgenic protein C was further characterized as follows:

A. ELISA

An enzyme-linked immunosorbent assay (ELISA) for 25 protein C was done as follows: Affinity-purified polyclonal antibody to human protein C (100 µl of 1 µg/ml in 0.1 M Na₂CO₃, pH 9.6) was added to each well of a 96-well microtiter plate, and the plates were incubated overnight at 4°C. The wells were then washed three times 30 with phosphate buffered saline (PBS) containing 0.05% Tween-20 and incubated with 100 µl of 1% bovine serum albumin (BSA), 0.05% Tween-20 in PBS at 4°C overnight. The plates were then rinsed several times with PBS, air dried and stored at 4°C. To assay samples, 100 µl of each sample 35 was incubated for 1 h at 37°C with a biotin-conjugated sheep polyclonal antibody to protein C (30 ng/ml) in PBS containing 1% BSA and 0.05% Tween-20. After incubation,

the wells were rinsed with PBS, and alkaline phosphatase activity was measured by the addition of 100 μ l of phosphatase substrate (Sigma, St. Louis, MO) in 10% diethanolamine, pH 9.8, containing 0.3 mM MgCl₂. The 5 absorbance at 405 nm was read on a micro-iter plate reader. Quantitation was by comparison with a standard curve using plasma-derived protein C quantitated by amino acid analysis.

10 B. Amino-Terminal Sequencing

Amino-terminal sequencing of the transgenic material was performed to ascertain the extent of prosequence removal and to evaluate the presence of gamma-carboxylation. There were three possible N-terminal 15 sequences of protein C. These were: 1) Prosequence which directs gamma-carboxylation and could have remained on the light chain if the first cleavage site was incompletely processed, 2) the light chain and 3) the heavy chain. N-terminal sequencing of protein C obtained from transgenic 20 milk should have contained only the latter two sequences if correct processing had occurred at both of the cleavage sites. Amino-terminal sequencing would have also been expected to reveal the presence of gamma-carboxylation in the light chain. There are nine sites of carboxylation in 25 the first twenty-nine amino acids of the light chain. On an analysis of released amino acids, the PTH-gamma carboxylic acid derivatives eluted from the HPLC column in the break-through and could therefore be analyzed. Thus, 30 a gamma carboxylic acid showed up on the amino-terminal sequence as a space rather than a glutamic acid.

The yields of amino acids in pmol released from the sequencing of approximately 27 pmol (1.4 μ l) of purified transgenic protein C corresponded well to those expected for an equimolar mixture of light and heavy 35 chains, and no obvious sequence was discernible for the prosequence. Moreover, no other aberrant sequences were

detected, thus indicating a lack of inappropriate proteolytic cleavages.

As stated previously, gamma-carboxylated glutamate residues were expected to sequence as blanks using standard instrument conditions. However, sequencing protein C gives a double sequence which must be deconvoluted using knowledge of the expected light and heavy chain sequences. Normally, if the light chain alone were sequenced the gla residues at positions six and seven would appear as blanks. However when sequenced as intact protein C, the heavy chain sequence contains a glutamate residue at position six. Therefore, the only indirect confirmation of the presence of a gla residue in the light chain was the absence of glutamate at position seven which was not 'over written' by a glutamate in the heavy chain (Figure 2). Two other indirect confirmations of the presence of gamma carboxylation of the transgenic product are described below.

20 C. Mass Analysis of the Purified Light Chain

The protein sequence of the transgenic-derived protein C precursor had been modified with an Arg-Arg-Lys-Arg (SEQ ID NO: 20) cleavage site between the light and heavy chains to promote more efficient cleavage of the single chain to 2-chain form. Western blot analysis of the transgenic protein C milk and examination of the purified protein C on reducing gels had already confirmed that efficient cleavage had occurred. Normally during secretion, but after cleavage of the plasma-derived material, the two basic amino acids at the carboxy-terminus of the light chain are trimmed back by a basic carboxypeptide. Establishing whether the carboxy-terminus of the transgenic protein C light chain had been processed to remove the two extra basic amino acids introduced by this modification, as well as the two natural ones, was achieved by measuring the mass of the purified light chain in a quadropole instrument using on-line liquid

chromatography and electro-spray ionization. In order to achieve this, all of the cysteine residues of protein C were reduced and alkylated, and then the two chains were separated by reversed-phase chromatography.

5

C1. Reductive Alkylation

Because protein C is heavily cross-linked for a molecule of approximately 52 kDa, with twelve disulfide bridges (17 of the 24 cysteines involved are in the light 10 chain), it was necessary to reductively alkylate the entire protein before attempting to separate the chains by reversed-phase chromatography. In view of the large number of cysteines in the light chain, alkylation was done with iodoacetamide, in place of the more commonly 15 used vinyl pyridine, to prevent the molecule from becoming excessively hydrophobic.

The transgenic protein C material (6 nmol of protein or 144 pmol of thiol) was reductively alkylated as follows: 0.5 mg of protein C (by ELISA) in 0.5 ml of TBS 20 was added to 50 μ l of 1 M Tris pH 8.0, 450 μ l water, 570 mg guanidinium chloride, and 10 μ l at 50 mg/ml DTT (0.3 μ mol representing a 20 fold excess of added thiol over cysteine thiol. The mixture was incubated for 2 hours at 37°C. After incubation, 20 μ l at 120 mg/ml iodoacetamide 25 (0.6 M representing a 2 fold excess over DTT on a molar basis) was added, and the mixture was incubated in the dark for one hour at 4°C. The reaction was quenched by adding 50 μ l at 50 mg/ml DTT representing a 2.5 fold excess over iodoacetamide. The sample (final volume 1.5 30 ml) was stored at -20°C until analysis.

D. Purification of the Light Chain

Purification of protein C light chain was achieved using a large pore polystyrene column with 35 divinyl benzene interactive groups (PLRP-S, 4000Å, 8 μ m, 2.1 mm ID: Polymer Laboratories, Shropshire, UK). The optimum conditions for separation of the heavy and light

chains were determined to be: solvent A (0.1% TFA) and solvent B (100% acetonitrile) at a flow of 0.5 ml/min with a detector wavelength of 215 nm and a gradient of 30 to 60% solvent B over 60 min.

5 Fractions were collected across the eluted peaks, and samples (10 µl) were analyzed by SDS PAGE on 4-20% gradient acrylamide gels under non-reducing conditions. The light chain (fractions 3 to 5) was completely resolved from both the heavy chain (fractions 7
10 to 9) and a single fraction (6) which contained a mixture of heavy chain and what appeared to be unglycosylated light chain.

A sample containing fully resolved light chain was prepared for deglycosylation by centrifugal
15 evaporation under reduced pressure at room temperature. Deglycosylation was carried out using peptide N-glycanase (PNGase; Oxford Glycosystems, Oxford, UK). The protein sample was redissolved in 50 µl of buffer and incubated overnight with 1 unit (5 µl) PNGase, according to
20 manufacturer's specifications.

The light chain was purified from reduced and alkylated plasma-derived protein C by the same method and deglycosylated for further analysis.

25 E. Analysis by Mass Spectroscopy

Samples of purified light chain were subjected to mass analysis using a liquid chromatography -
electrospray interface to a Sciex Quadrupole Mass Analyser (Sciex/Perkin Elmer, Toronto, CA). The LC system used a
30 0.5 mm ID column packed with PLRP-S 4000Å, 8µm resin (Polymer Laboratories). The solvent system contained buffer A (0.1% formic acid), buffer B (0.1% formic acid and a 5:2 (v/v) mixture of ethanol to propan-1-ol). The gradient used was from 5-60% buffer B over 35 minutes at a
35 flow rate of 25 µl per minute. The outflow of the column was linked via a UV detector to the mass spectrometer which was run in positive-ion mode.

The purified and deglycosylated transgenic light chain was analyzed and gave a relatively weak spectrum which was reconstructed to give two components with masses of 18,911.0 and 18,971.0. The plasma light chain was also 5 analyzed and gave a stronger signal with a single major component. The spectrum of the plasma light chain was reconstructed to give a single mass of 18,970.0.

The predicted mass for the light chain carrying nine gamma-carboxy glutamic acids, one β -hydroxy aspartic 10 acid and seventeen carbamidomethyl cysteine residues and ending with Leu₁₅₅ was 18966.9723, which is very close to the masses detected for the transgenic (18,971.0) and plasma-derived (18,970.0) light chains. The small 15 differences in mass were well within the accuracy limitations for this instrument, particularly with the LC delivery. This shows that the mass of the redirectively-alkylated and deglycosylated transgenic light chain is essentially identical to that for the plasma-derived protein C. This implies that both molecules have 20 undergone the same post-translational modifications and that the transgenic material is fully gamma carboxylated, has had all four basic amino acids trimmed back from the carboxy-terminus of the light chain and has single β hydroxy-alanine.

25

F. Activity Measurements

The activity of the transgenic protein C was compared with that of the plasma-derived material in a coagulation assay. First each sample of protein C, 30 quantitated by amino acid composition analysis, was activated by incubation with Protac, a snake venom (American Diagnostica Inc, Greenwich, CT) at a venom to protein ratio of 1 Unit Protac: 10 μ g protein C for 60 minutes at 37°C. Aliquots of the activated material were 35 then compared for their ability to prolong the clotting time of protein C depleted human plasma (Diagnostic Reagents Ltd) in the presence of activated partial

thromboplastin time reagent - cephalin from rabbit brain (Sigma) and calcium using a mechanical coagulometer (Diagnostica Stago, Asmieres, FR). A comparison of clotting times with various additions of transgenic and 5 plasma-derived protein C (Figure 3) shows that the two preparations had the same anti-coagulant activity per mg of protein.

In summary, results show that the sheep-derived transgenic protein C is correctly post-translationally 10 processed, with respect to gamma-carboxylation and probably beta-hydroxylation, and has anticoagulant activity fully equivalent to a high quality purified plasma standard. The results demonstrate that the C-terminal processing of the light chain, with the modified 15 RRKR cleavage site rather than the naturally occurring KR site, has the two extra basic amino acids removed along with the natural ones.

From the foregoing, it will be appreciated that, 20 although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
ANIMALS

(iii) NUMBER OF SEQUENCES: 25

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11725 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: join(3520..3630, 5093..5117, 5210..5347, 5450
..5584, 8253..8395, 9269..9386, 10516..11102)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AGCATCTTCT CATGATTTTA TGTATCAGAA ATTGGGATGG CATGTCATTG GGACAGCGTC	240
TTTTTCTTG TATGGTGGCA CATAAATACA TGTGTCTTAT AATTAATGGT ATTTAGATT	300
TGACGAAATA TGGAAATATTA CCTGTTGTGC TGATCTGGG CAAACTATAA TATCTCTGGG	360
CAAAATGTC CCCATCTGAA AACAGGGAC AACGTTCTC CCTCAGCCAG CCACTATGGG	420
GCTAAAATGA GACCACATCT GTCAAGGGTT TTGCCCTCAC CTCCCTCCCT GCTGGATGGC	480
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CAGTATCTCC ACGACCCGCC CCTGTGAGTC CCCCTCCAGG CAGGTCTATG AGGGGTGTGG	720
AGGGAGGGCT GCCCCCGGGA GAAGAGAGCT AGGTGGTGAT GAGGGCTGAA TCCCTCAGCC	780
AGGGTGCTCA ACAAGCCTGA GCTTGGGTA AAAGGACACA AGGCCCTCCA CAGGCCAGGC	840
CTGGCAGCCA CAGTCTCAGG TCCCTTGCC ATGGCCTCC CTCTTCCAG GCCAAEGGTC	900
CCCAGGCCA GGGCATTCC AACAGACAGT TTGGAGCCA GGACCCCTCCA TTCTCCCCAC	960
CCCACCTCCA CCTTTGGGGG TGTGGATTT GAACAAATCT CAGAAGCGGC CTCAGAGGGA	1020
GTCGGCAAGA A1GGAGAGCA GGGTCCGGTA GGGTGTGCAG AGGCCACGTG GCCTATCCAC	1080
TGGGGAGGGT TCCTTGATCT CTGGCCACCA GGGCTATCTC TGTGGCCTTT TGGAGCAACC	1140
TGGTGGTTTG GGGCAGGGGT TGAATTCCA GGCCTAAAAC CACACAGGCC TGGCCTTGAG	1200
TCCTGGCTCT GCGAGTAATG CATGGATGTA AACATGGAGA CCCAGGACCT TGCCCTAGTC	1260
TTCCGAGTCT GGTGCCTGCA GTGTACTGAT GGTGTGAGAC CCTACTCCG GAGGATGGGG	1320
GACAGAATCT GATCGATCCC CTGGGTTGGT GACTTCCCTG TGCAATCAAC GGAGACCAGC	1380
AAGGGTTGGA TTTTAATAA ACCACTAAC TCCTCCGAGT CTCAGTTCC CCCTCTATGA	1440
AATGGGGTTG ACAGCATTAA TAACTACCTC TTGGGTGGTT GTGAGCCTTA ACTGAAGTCA	1500
TAATATCTCA TGTTTACTGA GCATGAGCTA TGTGCAAAGC CTGTTTGAG AGCTTTATGT	1560
GGACTAACTC CTTAATTCT CACAACACCC TTTAAGGCAC AGATACACCA CGTTATTCCA	1620
TCCATTTAC AAATGAGGAA ACTGAGGCAT GGAGCAGTTA AGCATCTGC CCAACATTGC	1680
CCTCCAGTAA GTGCTGGAGC TGGAATTGCA ACCGTGCACT CTGGCTTCAT GGCCTGCCT	1740
GTGAATCCTG TAAAAATTGT TTGAAAGACA CCATGAGTGT CCAATCAACG TTAGCTATA	1800
TTCTCAGCCC AGTCATCAGA CCGGCAGAGG CAGCCACCCC ACTGTCCCCA GGGAGGACAC	1860
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GACCCCTCAAT TCCAGCTTCC GCCTGACGGC CAGCACACAG GGACAGCCCT TTCATTCCGC	2040
TTCCACCTGG GGGTGCAGGC AGAGCAGCAG CGGGGGTAGC ACTGCCCGA GCTCAGAAAGT	2100
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CCCCGGGACC CTTGTGGCCT CTACAAGGCC CTGGTGGCAT CTGCCAGGC CTTCACAGCT	2280
TCCACCATCT CTCTGAGCCC TGGGTGAGGT GAGGGGCAGA TGGGAATGGC AGGAATCAAC	2340
TGACAAGTCC CAGGTAGGCC AGCTGCCAGA GTGCCACACA GGGGCTGCCA GGGCAGGCAT	2400
GCGTGATGGC AGGGAGCCCC GCGATGACCT CCTAAAGCTC CCTCCTCCAC ACGGGGATGG	2460
TCACAGAGTC CCCTGGGCCT TCCCTCTCCA CCCACTCACT CCCTCAACTG TGAAGACCCC	2520
AGGCCAGGC TACCGTCCAC ACTATCCAGC ACAGCCTCCC CTACTCAAAT GCACACTGGC	2580
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GATTCTTGGG GAGGTCCGCA GGCACATGGG CCCCTAAAGC CACACCAGGC TGTTGGTTTC	2700
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GTGCCCTCAG CTCAGGCATA CCCTCCTCTA GGATGCCTT TCCCCCATCC CTTCTTGCTC	2820
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GAGCCCAGGA CACACCTGGG GACCCTCCT GGGTGATAGG TCTGTCTATC CTCCAGGTGT	2940
CCCTGCCCAA GGGGAGAAGC ATGGGAATA CTTGGTTGGG GGAGGAAAGG AAGACTGGGG	3000
GGATGTGTCA AGATGGGCT GCATGTGGTG TACTGGCAGA AGAGTGAGAG GATTTAACTT	3060
GGCAGCCTTT ACAGCAGCAG CCAGGGCTTG AGTACTTATC TCTGGGCCAG GCTGTATTGG	3120
ATGTTTACA TGACGGTCTC ATCCCCATGT TTTTGGATGA GTAAATTGAA CCTTAGAAAG	3180
GTAAAGACAC TGGCTCAAGG TCACACAGAG ATCGGGGTGG GGTTCACAGG GAGGCCTGTC	3240

CATCTCAGAG CAAGGCTTCG TCCTCCAATC GCCATCTGCT TCCTGGGAG GAAA/GAGCA 3300
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AGACCTTCCC AGGCTCTCCC AGCTCTGCTT CCTCAGACCC CCTCATGCC CCAGGCCCTC 3420
TTAGGCCCCT CACCAAGGTG AGCTCCCCTC CCTCCAAAAC CAGACTCAGT GTTCTCCAGC 3480
AGCGAGCGTG CCCACCAGGT GCTGCGGATC CGCAAACGT GCC AAC TCC TTC CTG 3534
GAG GAG CTC CGT CAC AGC AGC CTG GAG CGG GAG TGC ATA GAG GAG ATC 3582
TGT GAC TTC GAG GAG GCC AAG GAA ATT TTC CAA AAT GTG GAT GAC ACA 3630
GTAAGGCCAC CATGGGTCCA GAGGATGAGG CTCAGGGCG AGCTGGTAAC CAGCAGGGC 3690
CTCGAGGAGC AGGTGGGAC TCAATGCTGA GGCCCTCTTA GGAGTTGTGG GGGTGGCTGA 3750
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CCTCTTCCC CAGTGGCCTC CCTGGCAGAC ACCACAGTGA CTTCTGCAG GCACATATCT 4470
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AGCCAACGAC CATCGGGCGT CGATCCCTGT TTGTCTGGAA GCCCTCCCCCT CCCCTGCCCG 5010
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GACATTGCA TGACTCCCTG TGGTCAGCTA AGAGCACCAC TCCTTCCTGA AGCGGGGCCT	7194

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GGCTCGTCAC GTGCTGGTC CGGGATCACT GAGTCCATCC TGGCAGCTAT GCTCAGGGTG	8475

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CCCCCTCTTG CCAGGCATGG GGGAGATAGG AACCAACAAG TGGGAGTATT TGCCCTGGGG	8835
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CACCCCATTC CAG GTG GTC CTG CTG GAC TCA AAG AAG AAG CTG GCC TGC	9304
GGG GCA GTG CTC ATC CAC CCC TCC TGG GTG CTG ACA GCG GCC CAC T3C	9352
ATG GAT GAG TCC AAG AAG CTC CTT GTC AGG CTT G GTATGGGCTG	9396
GACCCAGGCA GAAGGGGGCT GCCAGAGGCC TGGGTAGGGG GACCAGGCAG GCTGTTAGG	9456
TTTGGGGGAC CCCGCTCCCC AGGTGCTTAA GCAAGAGGCT TCTTGAGCTC CACAGAAGGT	9516
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GCAGTAGGGG GTTCTCTGGT GCCCTCTCG AATCTGGCA CAGGTACCTG CACACACATG	9636
TTTGTGAGGG GCTACACAGA CCTTCACCTC TCCACTCCCA CTCATGAGGA GCAGGCTGTG	9696
TGGGCCTCAG CACCTTGGG TGCAGAGACC AGCAAGGCCT GGCCTCAGGG CTGTGCCTCC	9756
CACAGACTGA CAGGGATGGA GCTGTACAGA GGGAGCCCTA GCATCTGCCA AAGCCACAAG	9816

CTGCTTCCTT	AGCAGGGCTGG	GGGCTCCTAT	GCATTGGCCC	CGATCTATGG	CAATTTCTGG	9876
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AAATTACACAT	TTCCTACAGC	ATAATCTATG	CCAGTGGCCC	CGTGGGGCTT	GGCTTAGAAT	9996
TCCCAGGTGC	TCTTCCCAGG	GAACCATCAG	TCTGGACTGA	GAGGACCTTC	TCTCTCAGGT	10056
GGGACCCGGC	CCTGTCCCTCC	CTGGCAGTGC	CGTGTCTGG	GGGTCCCTCT	CTCTGGGTCT	10116
CACTGCCCTT	GGGGTCTCTC	CAGCTACCTT	TGCTCCATGT	TCTTTGTGG	CTCTGGTCTG	10176
TGTCTGGGGT	TTCCAGGGGT	CTCGGGCTTC	CCTGCTGCC	ATTCCCTCTC	TGGTCTCAGG	10236
GCTCCGTGAC	TCCTGAAAAC	CAACCAGCAT	CCTACCCCTT	TGGATTGACA	CCTGTTGGCC	10296
ACTCCTCTG	GCAGGAAAAG	TCACCGTTGA	TAGGGTTCCA	CGGCATAGAC	AGGTGGCTCC	10356
GCGCCAGTGC	CTGGGACGTG	TGGGTGCACA	GTCTCCGGGT	GAACCTCTT	CAGGCCCTCT	10416
CCCAGGCCTG	CAGGGGCACA	GCAGTGGGTG	GGCCTCAGGA	AAGTCCACT	GGGGAGAGGC	10476
TCCCCGCAGC	CCACTCTGAC	TGTGCCCTCT	GCCCTGCAG	GA GAG TAT	GAC CTG	10529
CGG CGC	TGG GAG	AAG TGG GAG	CTG GAC	CTG GAC	ATC AAG GAG	10577
GTC CAC	CCC AAC	TAC AGC AAG	AGC ACC	ACC GAC	AAT GAC ATC	10625
CTG CAC	CTG GCC	CAG CCC	GCC ACC	CTC TCG	CAG ACC ATA GTG	10673
TGC CTC	CCG GAC	AGC GGC	CTT GCA	GAG CGC	GAG CTC AAT CAG	10721
CAG GAG	ACC CTC	GTG ACG	GGC TGG	GGC TAC	CAC AGC AGC CGA	10769
GAG GCC	AAG AGA	AAC CGC	ACC TTC	GTC CTC	AAC TTC ATC AAG	10817
GTG GTC	CCG CAC	AAT GAG	TGC AGC	GAG GTC	ATG AGC AAC ATG	10865
GAG AAC	ATG CTG	TGT GCG	GGC ATC	CTC GGG	GAC CGG CAG GAT	10913
GAG GGC	GAC AGT	GGG GGG	CCC ATG	GTC GCC	TCC TTC CAC GGC	10961
TTC CTG	GTG GGC	CTG GTG	AGC TGG	GGT GAG	GGC TGT GGG CTC	11009

AAC TAC GGC GTT TAC ACC AAA GTC AGC CGC TAC CTC GAC TGG ATC CAT	11057
GGG CAC ATC AGA GAC AAG GAA GCC CCC CAG AAG AGC TGG GCA CCT	11102
TAGCGACCCCT CCCTGCAGGG CTGGCTTTT GCATGGCAAT GGATGGGACA TTAAAGGGAC	11162
ATGTAACAAG CACACGGCC TGCTGTTCTG TCCTTCCATC CCTCTTTGG GCTCTTCTGG	11222
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ACTCCTAGAG CAACTCTGTG GGGTGGGAG GAGCAGATCC AAGTTTGCG GGGTCTAAAG	11342
CTGTGTGTGT TGAGGGGGAT ACTCTGTTA TGAAAAAGAA TAAAAAACAC AACCAAGAAG	11402
CCACTAGAGC CTTTCCAGG GCTTGGGAA GAGCCTGTGC AAGCCGGGA TGCTGAGGT	11462
GAGGCTTGAC CAGCTTCCA GCTAGCCCAG CTATGAGGTA GACATGTTA GCTCATATCA	11522
CAGAGGAGGA AACTGAGGGG TCTGAAAGGT TTACATGGTG GAGCCAGGAT TCAAACTAG	11582
GTCTGACTCC AAAACCCAGG TGCTTTTTC TGTTCTCCAC TGTCCTGGAG GACAGCTGTT	11642
TCGACGGTGC TCAGTGTGGA GGCCACTATT AGCTCTGTAG GGAAGCAGCC AGAGACCCAG	11702
AAAGTGTGGG TTCAGCCAG AAT	11725

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile			
1	5	10	15

Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg		
20	25	30

Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu
35 40 45

Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys
50 55 60

Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu
65 70 75 80

Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro
85 90 95

Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile
100 105 110

Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly
115 120 125

Arg Phe Cys Gln Arg Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn
130 135 140

Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys
145 150 155 160

Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His
165 170 175

Pro Ala Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys
180 185 190

Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val
195 200 205

Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro
210 215 220

Trp Gln Val Val Leu Leu Asp Ser Lys Lys Leu Ala Cys Gly Ala
225 230 235 240

Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp
245 250 255

Glu Ser Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg
260 265 270

Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys Glu Val Phe Val His
275 280 285

Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His
290 295 300

Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu
305 310 315 320

Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu
325 330 335

Thr Leu Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala
340 345 350

Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val
355 360 365

Pro His Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn
370 375 380

Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly
385 390 395 400

Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu
405 410 415

Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr
420 425 430

Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His
435 440 445

Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala
450 455 460

(2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..1380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TGG CAG CTC ACA AGC CTC CTG CTG TTC GTG GCC ACC TGG GGA ATT	48
Met Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile	
1 5 10 15	
TCC GGC ACA CCA GCT CCT CTT GAC TCA GTG TTC TCC AGC AGC GAG CGT	96
Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg	
20 25 30	
GCC CAC CAG GTG CTG CGG ATC CGC AAA CGT GCC AAC TCC TTC CTG GAG	144
Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu	
35 40 45	
GAG CTC CGT CAC AGC AGC CTG GAG CGG GAG TGC ATA GAG GAG ATC TGT	192
Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys	
50 55 60	
GAC TTC GAG GAG GCC AAG GAA ATT TTC CAA AAT GTG GAT GAC ACA CTG	240
Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu	
65 70 75 80	
GCC TTC TGG TCC AAG CAC GTC GAC GGT GAC CAG TGC TTG GTC TTG CCC	288
Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro	
85 90 95	
TTG GAG CAC CCG TGC GCC AGC CTG TGC GGG CAC GGC ACG TGC ATC	336
Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile	
100 105 110	
GAC GGC ATC GGC AGC TTC AGC TGC GAC TGC CGC AGC GGC TGG GAG GGC	384
Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly	
115 120 125	
CGC TTC TGC CAG CGC GAG GTG AGC TTC CTC AAT TGC TCT CTG GAC AAC	432
Arg Phe Cys Gln Arg Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn	
130 135 140	

GGC GGC TGC ACG CAT TAC TGC CTA GAG GAG GTG GGC TGG CGG CCC TGT Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys 145 150 155 160	480
AGC TGT GCG CCT GGC TAC AAG CTG GGG GAC GAC CTC CTG CAG TGT CAC Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His 165 170 175	528
CCC GCA GTG AAG TTC CCT TGT GGG AGG CCC TGG AAG CGG ATG GAG AAG Pro Ala Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys 180 185 190	576
AAG CGC AGT CAC CTG AAA CGA GAC ACA GAA GAC CAA GAA GAC CAA GTA Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val 195 200 205	624
GAT CCG CGG CTC ATT GAT GGG AAG ATG ACC AGG CGG GGA GAC AGC CCC Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro 210 215 220	672
TGG CAG GTG GTC CTG CTG GAC TCA AAG AAG CTG GCC TGC GGG GCA Trp Gln Val Val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala 225 230 235 240	720
GTG CTC ATC CAC CCC TCC TGG GTG CTG ACA GCG GCC CAC TGC ATG GAT Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp 245 250 255	768
GAG TCC AAG AAG CTC CTT GTC AGG CTT GGA GAG TAT GAC CTG CGG CGC Glu Ser Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg 260 265 270	816
TGG GAG AAG TGG GAG CTG GAC CTG GAC ATC AAG GAG GTC TIC GTC CAC Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys Glu Val Phe Val His 275 280 285	864
CCC AAC TAC AGC AAG AGC ACC ACC GAC AAT GAC ATC GCA CTG CTG CAC Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His 290 295 300	912
CTG GCC CAG CCC GCC ACC CTC TCG CAG ACC ATA GTG CCC ATC TGC CTC Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu 305 310 315 320	960

CCG GAC AGC GGC CTT GCA GAG CGC GAG CTC AAT CAG GCC GGC CAG GAG Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu 325 330 335	1008
ACC CTC GTG ACG GGC TGG GGC TAC CAC AGC AGC CGA GAG AAG GAG GGC Thr Leu Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala 340 345 350	1056
AAG AGA AAC CGC ACC TTC GTC CTC AAC TTC ATC AAG ATT CCC GTG GTC Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val 355 360 365	1104
CCG CAC AAT GAG TGC AGC GAG GTC ATG AGC AAC ATG GTG TCT GAG AAC Pro His Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn 370 375 380	1152
ATG CTG TGT GCG GGC ATC CTC GGG GAC CGG CAG GAT GCC TGC GAG GGC Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly 385 390 395 400	1200
GAC AGT GGG GGG CCC ATG GTC GCC TCC TTC CAC GGC ACC TGG TTC CTG Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu 405 410 415	1248
GTG GGC CTG GTG AGC TGG GGT CAG GGC TGT GGG CTC CTT CAC AAC TAC Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr 420 425 430	1296
GGC GTT TAC ACC AAA GTC AGC CGC TAC CTC GAC TGG ATC CAT GGG CAC Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His 435 440 445	1344
ATC AGA GAC AAG GAA GCC CCC CAG AAG AGC TGG GCA CCTTAG Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala 450 455 460	1386

(2) INFORMATION FOR SEQ ID NO.4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 460 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION SEQ ID NO:4:

Met Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile
1 5 10 15

Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg
20 25 30

Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu
35 40 45

Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys
50 55 60

Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu
65 70 75 80

Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro
85 90 95

Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile
100 105 110

Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly
115 120 125

Arg Phe Cys Gln Arg Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn
130 135 140

Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys
145 150 155 160

Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His
165 170 175

Pro Ala Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys
180 185 190

Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val
195 200 205

Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro
210 215 220

Trp Gln Val Val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala
225 230 235 240

Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp
245 250 255

Glu Ser Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg
260 265 270

Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys Glu Val Phe Val His
275 280 285

Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His
290 295 300

Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu
305 310 315 320

Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu
325 330 335

Thr Leu Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala
340 345 350

Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val
355 360 365

Pro His Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn
370 375 380

Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly
385 390 395 400

Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu
405 410 415

Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr
420 425 430

Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His
435 440 445

Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala
450 455 460

(2) INFORMATION FOR SEQ ID NO:5:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACGCGTGTG	ACCTGCAGGT	CAACGGATCT	CTGTGTCTGT	TTTCATGT	TA GTACCA	CACT	60
GT	TTTGGTGG	CTGTAGCTT	CAGCTACAGT	CTGAAGTCAT	AAAGCCTGGT	ACCTCCAGCT	120
CTG	TTCTCTC	TCAAGATTGT	GTTCTGCTGT	TTGGGTCTTT	AGTGTCTCCA	CACAATT	180
AGA	ATTGTTT	GTTCTAGTTC	TGTGAAAAAT	GATGCTGGTA	TTTGATAAG	GATTGCATTG	240
AAT	CTGTAAA	GCTACAGATA	TAGTCATGG	GTAGTACAGT	CACTTTAAC	ATATTAACTC	300
TTC	CACATCTG	TGAGCATGAT	ATATTTCCC	CCTCTATATC	ATCTTCATT	CCTCCATCA	360
GT	TTTCTTCA	TTGCAGTTT	CTGAGTACAG	GTCTTACACC	TCCTGGTTA	GAGTCATTCC	420
TCAGT	ATTCTTGA	TACAATTG	AATGAGGTAA	TTTCTTAGT	TTCTCTTCT	480	
GATAG	CTCAT	TGTTAGTGT	TATATAGAA	ASCAACAGAT	TTCTATGTAT	TAATTTGTA	540
TCCTG	CAACA	GATTCTATG	TATTAATT	GTATCCTGCT	ACTTACGGA	ATTCACTTAT	600
TAGCT	TTTG	GTGACATCTT	GAGGATTTTC	TGAAGAAAAT	GGCATGGTAT	GGTAGGACAA	660
GGTGT	CATCTGAAA	CAGTGGCACT	TTCCCTCTT	CCCTTCCAAC	CTGGATTCT	720	
TTGATT	CTT	TCTGTCTGAG	TACGACTAGG	ATCCCCATA	CTATACCGAA	TAAGGTGGC	780
AAGAGTGGAC	ATCCTTGTCT	TATTTCTG	ACCTTAGAGG	AAATGCTTTC	AGTTTTTCAC	840	
CATTAATTAT	AATGTTACT	GTGGGCTTGT	CATATGTGGC	CTTCATTATA	TGGAEGTCTA	900	
TTCCCTCTAT	ACCCACCTTG	TTGAGAGTT	TTATCATAAA	AGTATGTGA	ATTTTGTCAA	960	
AAGTTTTTCC	TGCATCTATT	GAGATGATT	TTACTCTTCA	ATTCAATT	GATTTTTATT	1020	

CTTCATTTG TTAATGATT CCATTCTCA ATTTGTTAAC GTGGTATATC ACATTGATTG	1080
ATTTGTGGAT ACCTTTGTAT CCCTGGGATA AACCTCACTT GATCATGAGC TTTCAATGTA	1140
TTTTGAATT CACTTGCTA ATATTCTGT1 GGGTATTTT GCATCTCTAT TCATCAATGA	1200
TATTGGCCTA AGAAAGGTTT TGTCTGTTT TAGTATCAGG GTGATGCTGG CCTCATAGAG	1260
AGAGTTAGA AGCATTCTCCT CCTCTTTGAT TTTTGGAAAT AGTTTGAGTA GGATAGGTAT	1320
TAACTCTCT TAAATGTTT GGGGACTTCC CTGGTGAGCC GGTGGTTGAG AATCCGCCTC	1380
AGGGATGTGG GTTGTATCCC TGGTCAGGGA ACCATTAATA AGATCCACA TGCTGCAGGC	1440
AACAAGCCCC CAAGCTGCAA CCACTGAGCT GCAACCGCTG CAGTGCCAAC AGGCCACGAC	1500
CAGAGAAAGC CCACATACAG CAGGGAAAGAC CCAGCACAAC CGGAAAAGG AGTTTGGTGG	1560
AATACAGCTG TGAAGCCGTC TGGTCCTGGA CTCTGCTTG AGGAAATT TTAAAAATTAA	1620
TTGATTCAAT TTCATTACTG GTAACTGGTC TGTTCATATT TTCTATTCTC TCCGGGTTCA	1680
GTCTTGGGAG ATTGTACATG CCTAGGAATG TGTCCGTTTC TTCTAGGTTG TCCATTCTAT	1740
TGGACATGCA TGGGAGCACA CAGCACCGAC CAGCGAGACT CATGCTGGCT TCCTGGGCC	1800
AGGCTGGGCC CCCAAGCAGC ATGCACTCT AGAGTGTGTG AAAGCCACT GACCTGCC	1860
AGCCCCACAA TTTCATTCTG AGAAAGTGATT CCTTGCTCT GCACTTACAG GCCCAGGATC	1920
TGACCTGCTT CTGAGGGAGCA GGGSTTTGG CAGGACGGGG AGATGCTGAG AGCCGACGGG	1980
GGTCCAGGTC CCCTCCCAGG CCCCCCTGTC TGGGGCAGCC CTTGGGAAAG ATTGCCAG	2040
TCTCCCTCT ACAGTGGTCA GTCCCAGCTG CCCCAGGCCA GAGCTGCTT ATTCCGTCT	2100
CTCTCTCTGG ATGGTATTCT CTGGAAGCTG AAGGTTCTG AAGTTATGAA TAGCTTGTCC	2160
CTGAAGGGCA TGGTTTGTTG TCAAGGTTCA CAGGAACCTG GGAGACCCCTG CAGCTCAGAC	2220
GTCCCGAGAT TGGTGGCACC CAGATTCCT AAGCTCGCTG GGGAACAGGG CGCTTGTTC	2280
TCCCTGGCTG ACCTCCCTCC TCCCTGCATC ACCCAGTTCT GAAAGCAGAG CGGTGCTGGG	2340

GTCACAGCCT	CTCGCATCTA	ACGCCGGTGT	CCAAACCACC	CGTGCTGGTG	TTCGGGGGGC	2400
TACCTATGGG	GAAGGGCTTC	TCACTGCAGT	GGTGCCCCCC	GTCCCCCTCTG	AGATCAGAAG	2460
TCCCAGTCCG	GACGTCAAAC	AGGCCGAGCT	CCCTCCAGAG	GCTCCAGGGA	GGGATCCTTG	2520
CCCCCCCCGCT	GCTGCCTCCA	GCTCCTGGTG	CCGCACCCCTT	GAGCCTGATC	TTGTAGACGC	2580
CTCAGTCTAG	TCTCTGCCTC	CGTGTTACA	CGCCTTCTCC	CCATGTCCCC	TCCGTGTCCC	2640
CGTTTCTCT	CACAAGGACA	CCGGACATTA	GATTAGCCCC	TGTTCCAGCC	TCACCTGAAC	2700
AGCTCACATC	TGTAAAGACC	TAGATTCAA	ACAAGATTCC	AACCTGAAGT	TCCCAGGTGGA	2760
TGTGAGTTCT	GGGGCGACAT	CCCTCAACCC	CATCACAGCT	TGCAGTTCAT	CGCAAAACAT	2820
GGAACCTGGG	GTTTATCGTA	AAACCCAGGT	TCTTCATGAA	ACACTGAGCT	TCGAGGCTTG	2880
TTGCAAGAAT	TAAAGGTGCT	AATAACAGATC	AGGGCAAGGA	CTGAAGCTGG	CTAACCTCTCC	2940
TCTTTCCATC	ACAGGAAAGG	GGGGCCTGGG	GGCGGCTGG	GGTCTGCTCC	CGTGAGTGAG	3000
CTCTTCTCTG	CTACAGTCAC	CAACAGTCTC	TCTGGGAAGG	AAACCAGAGG	CCAGAGAGCA	3060
AGCCGGAGCT	AGTTAGGAG	ACCCCTGAAC	CTCCACCCAA	GATGCTGACC	AGCCAGCGGG	3120
CCCCCTGGAA	AGACCTACA	GTTCAAGGGG	GAAGAGGGGC	TGACCCGCCA	GGTCCCTGCT	3180
ATCAGGAGAC	ATCCCCGCTA	TCAGGAGATT	CCCCCACCTT	GCTCCGTTTC	CCCTATCCCA	3240
ATACGCCAC	CCCACCCCTG	TGATGAGCAG	TTTAGTCACT	TAGAATGTCA	ACTGAAGGCT	3300
TTTGATCCC	CTTTGCCAGA	GGCACACAAGGC	ACCCACAGCC	TGCTGGGTAC	CGACGCCCAT	3360
GTGGATTCA	CCAGGAGGCC	TGTCCTGCAC	CCTCCCTGCT	CGGGCCCCCT	CTGTGCTCAG	3420
CAACACACCC	AGCACCCAGCA	TTCCCGCTGC	TCCTGAGGTC	TGCAGGCAGC	TCGCTGTAGC	3480
CTGAGCGGTG	TGGAGGGAAAG	TGTCCTGGGA	GATTTAAAT	GTGAGAGGCG	GGAGG-GGGA	3540
GGTTGGGCC	TGTGGGCCTG	CCCATCCAC	GTGCCTGCAT	TAGCCCCAGT	GCTGC-CAGC	3600
CGTGCCCCCG	CCGCAGGGGT	CAGGTCACTT	TCCCGTCTG	GGGTTATTAT	GACTCTGTC	3660
ATTGCCATTG	CCATTTTGC	TACCTAACT	GGGCAGCAGG	TGCTTGAGA	GCCCT(GATA	3720

CCGACCAGGT CCTCCCTCGG AGCTCGACCT GAACCCATG TCACCCCTGC CCCAGCCTGC	3780
AGAGGGTGGG TGACTGCAGA GATCCCTCA CCCAAGGCCA CGGTACATG GTTTGGAGGA	3840
GCTGGTCCCC AAGGCAGAGG CCACCCCTCA GGACACACCT GTCCCCAGTG CTGGCTCTGA	3900
CCTGTCCCTG TCTAAGAGGC TGACCCCGGA AGTGTCCCTG GCACTGGCAG CCAGCCTGGA	3960
CCCAGAGTCC AGACACCCAC CTGTCCCCC GCTTCTGGGG TCTACCAGGA ACCGCTAGG	4020
CCCAGAGGGG ACTTCCTGCT TGGCCTTGGA TGGAAAGAAGG CCTCCTATTG TCCTCGTAGA	4080
GGAAGCCACC CCGGGGCCTG AGGATGAGCC AAGTGGGATT CCGGGAACCG CGTGGCTGGG	4140
GGCCCAGCCC GGGCTGGCTG GCCTGCATGC CTCCGTATA AGGCCCCAAG CCTGCTGTCT	4200
CAGCCCTCCA CTCCCTGCAG AGCTCAGAAG CACGACCCCA GGGATATCCC TGCAAGCCATG	4260
AAGTGCCTCC TGCTTGCCTT GGGCCTGGCC CTCGCCTGTG GCGTCCAGGC CATCATCGTC	4320
ACCCAGACCA TGAAAGGCCT GGACATCCAG AAGGTTCGAG GGTTGGCCGG GTGGGTGAGT	4380
TGCAGGGCGG GCAGGGGAGC TGGGCCTCAG AGAGCCAAGA GAGGCTGTGA CGTTGGGTTC	4440
CCATCAGTCA GCTAGGGCCA CCTGACAAAT CCCCCTGGG GCAGCTCAA CCAGGGGTTC	4500
ACTGTCTGC ATTCTGGAGG CTGGAAAGCCC AAGATCCAGG TGTTGGCAGG GCTGGCTTCT	4560
CCTGCAGGGCGG CTCTCTGGGG AGCAGACGGC CGTCTCTCC AGTCCTCTGC GCGCCCTGAT	4620
TTCCTCTTCC TGTGAGGCCA CCAGGCCTGC TGGAAACACG CCTGCCTGCG CAGCTTCACA	4680
CGACCTTTGT CATCTCTTA AAGGCCATGT CTCCAGAGTC ATGTGTTGAA GTTCTGGGGG	4740
TTAGTGGGAC ACAGTTCAGC CCCTAAAAGA GTCTCTCTGC CCCTCAAATT TTCCCCACCT	4800
CCAGCCATGT CTCCCCAAGA TCCAAATGTT GCTACATGTG GGGGGCTCA TCTGGGTCCC	4860
TCTTTGGGTT CAGTGTGAGT CTGGGGAGAG CATTCCCCAG GGTGCAGAGT TGGGGGGAGT	4920
ATCTCAGGGC TGCCCCAGGCC GGGGTGGGAC AGAGAGCCCA CTGTGGGGCT GGGGGCCCT	4980
TCCCCACCCCA AGAGTGCAAC TCAAGGTCCC TCTCCAGGTG GCGGGGACTT GGCACTCCTT	5040

GGCTATGGCG GCCAGCGACA TCTCCCTGCT GGATGCCAG AGTGCCCCC TGAGAGTGT 5100
CGTGGAGGAG CTGAAGCCA CCCCCGAGGG CAAACCTGGAG ATCCTGCTGC AGAAAATGGTG 5160
GGCGTCTCTC CCCAACATGG AACCCCCACT CCCCAGGGCT GTGGACCCCC CGGGGGGTGG 5220
GGTGCAGGAG GGACCAAGGGC CCCAGGGCTG GGAAAGAGGG CTCAGAGTTT ACTGETACCC 5280
GGCGCTCCAC CCAAGGCTGC CCACCCAGGG CTTTTTTTTT TTTAAACTT TTATTAATT 5340
GATGCTTCAG AACATCATCA AACAAATGAA CATAAAACAT TCATTTTGT TTACTTGGAA 5400
GGGGAGATAA AATCCTCTGA AGTGGAAATG CATAGCAAAG ATACATACAA TGAGGCAGGT 5460
ATTCTGAATT CCCTGTTAGT CTGAGGATTA CAAAGTGTATT TGAGCAACAG AGAGACATT 5520
TCATCATTTC TAGTCTGAAC ACCTCAGTAT CTAAATGAA CAAGAAGTCC TGGAAACGAA 5580
GCAGTGTGGG GATAGGCCCG TGTGAAGGCT GCTGGGAGGC AGCAGACCTG GGTCTTCGGG 5640
CTCAAGCAGT TCCCCCTTAC AGCCCTGTCC ACCTCAGACG GGGGTCAAGGG TGCAGGAGAG 5700
AGCTGGATGG GTGTGGGGC AGAGATGGGG ACCTGAACCC CAGGGCTGCC TTTTGGGGT 5760
GCCTGTGGTC AAGGCTCTCC CTGACCTTT CTCTCTGGCT TCATCTGACT TCTCTGGCC 5820
CATCCACCCG GTCCCCGTG GCCTGAGGTG ACAGTGAGTG CGCCGAGGCT AGTTGGCCAG 5880
CTGGCTCTA TGCCCATGCC ACCCCCCCTCC AGCCCTCCTG GGCCAGCTTC TGCCCTGGC 5940
CCTCAGTTCA TCCTGATGAA AATGGTCCAT GCCAATGGCT CAGAAAGCAG CTGTCTTCA 6000
GGGAGAACGG CGAGTGTGCT CAGAAGAAGA TTATTGCAGA AAAAACCAAG ATCCCTGCGG 6060
TGTTCAAGAT CGATGGTGAG TCCGGGTCCC TGGGGGACAC CCACCAACCC CGCCCGGG 6120
GACTGTGGAC AGGTTCAAGGG GGCTGGCGTC GGGCCCTGGG ATGCTAAGGG ACTGGTGGTG 6180
ATGAAGACAC TGCCCTGACA CCTGCTTACAC TTGCCTCCCC TGCCACCTGC CGGGGCCCTT 6240
GGGGCGGTGG CCATGGGCAG GTCCCCGGCTG GCGGGCTAAC CCACCAAGGGT GACACCCGAG 6300
CTCTCTTTGC TGGGGGGCGG GGGGTGCTCT GGGCCCTCAG GCTGAGCTCA GGAGGTAACCT 6360
GTGCCCTCCC AGGGGTAACC GAGAGCCGTT GCCCACTCCA GGGGCCAGG TGCCCCACGA 6420

CCCCAGCCCC	CTCCACAGCT	CCTTCATCTC	CTGGAGACAA	ACTCTGTCCG	CCCTCGCTCA	6480
TTCACTTGT	CGTCCTAAAT	CCGAGATGAT	AAAGCTTCGA	GGGGGGGTTG	GGGTTCCATC	6540
AGGGCTGCC	TTCCGCCGGG	CAGCCTGGC	CACATCTGCC	CTTGGCCCCC	TCAGGACTCA	6600
CTCTGACTGG	AGGCCCTGCA	CTGACTGACG	CCAGGGTGCC	CAGCCCAGGG	TCTCTGGCGC	6660
CATCCAGCTG	CACTGGGTTT	GGGTGCTGGT	CCTGCCCCCA	AGCTGCCCGG	ACACCACAGG	6720
CAGCCGGGGC	TGCCCACTGG	CCTCGGTCA	GGTGAGCCCC	AGCTGCCCCC	GCTCAGGGCT	6780
TGCCCCGACA	ATGACCCCCAT	CCTCAGGACG	CACCCCCCTT	CCCTTGCTGG	GCAGTGTCCA	6840
GCCCCACCCG	AGATCGGGGG	AAGCCCTATT	TCTTGACAAAC	TCCAGTCCT	GGGGGAGGGG	6900
GCC	CAGACT	GAGTGGTGAG	TGTTCCCAAG	TCCAGGAGGT	GGTGGAGGGT	6960
CCAGAGTTGA	CAGTGAGGGC	TTCCCTGGCC	CCATGCGCCT	GGCAGTGGCA	GCAGGGAAGA	7020
GGAAGCACCA	TTTCAGGGGT	GGGGGATGCC	AGAGGCCTC	CCCACCCCGT	CTTCGCCGGG	7080
TGGTGACCCC	GGGGGAGCCC	CGCTGGTCGT	GGAGGGTGCT	GGGGGCTGAC	TAGCAACCCC	7140
TCCCCCCCCG	TTGGAACCTCA	CTTTTCTCCC	GTCTTGACCG	CGTCCAGCCT	TGAATGAGAA	7200
CAAAGTCCTT	GTGCTGGACA	CCGACTACAA	AAAGTACCTG	CTCTTCTGCA	TGGAAAACAG	7260
TGCTGAGCCC	GAGCAAAGCC	TGGCCTGCCA	GTGCCTGGGT	GGGTGCCAAC	CCTGGCTGCC	7320
CAGGGAGACC	AGCTGCGTGG	TCCTTGCTGC	AACAGGGGGT	GGGGGGTGGG	AGCTTGATCC	7380
CCAGGAGGAG	GAGGGGTGGG	GGGTCCCTGA	GTCCCGCCAG	GAGAGAGTGG	TCGCATACCG	7440
GGAGCCAGTC	TGCTGTGGC	CTGTGGGTGG	CTGGGGACGG	GGGCCAGACA	CACAGGCCGG	7500
GAGACGGGTG	GGCTGCAGAA	CTGTGACTGG	TGTGACCGTC	GCGATGGGGC	CGGTGGTCAC	7560
TGAATCTAAC	AGCCTTGT	ACCGGGGAGT	TTCAATTATT	TCCAAAATA	AGAACTCAGG	7620
TACAAAGCCA	TCTTCACT	ATCACATCCT	AAAAACAAAT	GGCAGGTGAC	ATTTTCTGTG	7680
CCGTAGCAGT	CCCACTGGGC	ATTTTCAGGG	CCCCCTGTGCC	AGGGGGGCCG	GGGCATCGGC	7740

GAGTGGAGGC	TCCTGGCTGT	GTCAGCCGGC	CCAGGGGAG	GAAGGGACCC	GGACAGCCAG	7800
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GGGAGGGGAA	CTAGGCCAAG	GGGGAAGGGC	AGGTGCTCTG	GAGGGCAAGG	GCAGACCTGC	7920
AGACCAACCT	GGGGAGCAGG	GACTGACCCC	CGTCCCTGCC	CCATAGTCAG	GACCCGGAG	7980
GTGGACAACG	AGGCCCTGGA	GAAATTGAC	AAAGCCCTCA	AGGCCCTGCC	CATGCACATC	8040
CGGCTTGCT	TCAACCCGAC	CCAGCTGGAG	GGTGAGCACC	CAGGCCCCGC	CCTTCCCCAG	8100
GGCAGGAGCC	ACCCGGCCCC	GGGACGACCT	CCTCCCATGG	TGACCCCCAG	CTCCCCAGGC	8160
CTCCCAGGAG	GAAGGGGTGG	GGTGAGCAC	CCCGTGGGGG	CCCCCTCCCC	ACCCCTGCC	8220
AGGCCTCTCT	TCCCAGGAGTG	TCCAGTCCC	TCCTGACCCC	CCCATGACTC	TCCCTCCCC	8280
ACAGGGCAGT	GCCACGTCTA	GGTGAGCCCC	TGCCGGTGCC	TCTGGGGTAA	GCTGCCGTGCC	8340
CTGCCCCACG	TCCTGGGCAC	ACACATGGGG	TAGGGGGTCT	TGGTGGGGCC	TGGGACCCCCA	8400
CATCAGGCC	TGGGGTCCCC	CCTGTGAGAA	TGGCTGGAAG	CTGGGGTCCC	TCCTGGCGAC	8460
TGCAGAGCTG	GCTGGCCGCG	TGCCACTCTT	GTGGGTGACC	TGTGTCTGG	CCTCACACAC	8520
TGACCTCTC	CAGCTCCTTC	CAGCAGAGCT	AAGGCTAAGT	GAGCCAGAAT	GGTACCTAAG	8580
GCGAGGCTAG	CGGTCCCTCT	CCCGAGGAGG	GGCTGTCTG	GAACCACCAAG	CCATGGAGAG	8640
GCTGGCAAGG	GTCTGGCAGG	TGCCCCAGGA	ATCACAGGGG	GGCCCCATGT	CCATTCTAGG	8700
GCCCCGGAGC	CTTGGACTCC	TCTGGGGACA	GACGACGTCA	CCACCGCCCC	CCCCCCATCA	8760
GGGGGACTAG	AAGGGACCAAG	GACTGCAGTC	ACCCCTCCTG	GGACCCAGGC	CCCTCCAGGC	8820
CCCTCCTGGG	GCTCCTGCTC	TGGCAGCTT	CTCCTTCACC	AATAAAGGCA	AAACCTGTG	8880
CTCTCCCTTC	TGAGTCTTTC	CTGGACGACG	GGCAGGGGGT	GGAGAAGTGG	TGGGGAGGG	8940
GTCTGGCTCA	GAGGATGACA	GGGGGCTGG	GATCCAGGGC	GTCTGCATCA	CAGTCTTGTG	9000
ACAACTGGGG	GCCCCACACAC	ATCACTGCGG	CTCTTGAAA	CTTCAGGAA	CCAGGGAGGG	9060
ACTCGGCAGA	GACATCTGCC	AGTTCACTTG	GAGTGTTCAG	TCAACACCCA	AACTCCACAA	9120

AGGACAGAAA	GTGGAAAATG	GCTGTCTCTT	AGTCTAATAA	ATATTGATAT	GAAACTCAAG	9180
TTGCTCATGG	ATCAATATGC	CTTTATGATC	CAGCCAGCCA	CTACTGTCGT	ATCAACTCAT	9240
GTACCCAAAC	GCACTGATCT	GTCTGGCTAA	TGATGAGAGA	TTCCCAGTAG	AGAGCTGGCA	9300
AGAGGTCACA	GTGAGAACTG	TCTGCACACA	CAGCAGAGTC	CACCAAGTCAT	CCTAAGGAGA	9360
TCAGTCCTGG	TGTTCATTTGG	AGGACTGATG	TTGAAGCTGA	AACTCCAATG	CTTTGGCCAC	9420
CTGATGTGAA	GAGCTGACTC	ATTGAAAAG	ACCCCTGATGC	TGGGAAAGAT	TGAGGGCAGG	9480
AGGAGAAGGG	GACGACAGAG	GATGAGATGG	TTGGATGGCA	TCACCAACAC	AATGGACATG	9540
GGTTTGGGTG	GACTCCAGGA	GTTGGTGTG	GACAGGGAGG	CCTGGCGTGC	TACGGAAGCG	9600
GTTTATGGGG	TCACAAAGAC	TGAGTGACTG	AACTGAGCTG	AACTGAATGG	AAATGAGGTA	9660
TACAGCAAAG	TGGGGATTTT	TTAGATAATA	AGAATATAACA	CATAACATAG	TGTATACTCA	9720
TATTTTATG	CATACCTGAA	TGCTCAGTCA	CTCAGTCGTA	TCTGACTCTG	TGACCTATGG	9780
ACCGTAGCCT	TCCAGGTTTC	TTCTGTCCAC	AGAATTCTCC	AAGGCAAGAA	TACTGGAGTG	9840
GGTAGCCATT	TCCTCCTCCA	GGGGATCCTC	CCGACCCAGG	GATTGAACCG	GCATCTCCTG	9900
TATTGGCAGG	TGGATTCTTT	ACCACTGTGC	CACCAGGGAA	GCCCCTGTTA	CTCTCTATGT	9960
CCCACCTTAAT	TACCAAAGCT	GCTCCAAGAA	AAAGCCCCTG	TGCCCTCTGA	GCTTCCCGGC	10020
CTGCAGAGGG	TGGTGGGGGT	AGACTGTGAC	CTGGGAACAC	CCTCCCGCTT	CAGGACTCCC	10080
GGGCCACGTG	ACCCACAGTC	CTGCAGACAG	CCGGGTAGCT	CTGCTCTTCA	AGGCTCATTA	10140
TCTTTAAAAA	AAACTGAGGT	CTATTTGTG	ACTTCGCTGC	CGTAACTTCT	GAACATCCAG	10200
TGCGATGGAC	AGGACCTCCT	CCCCAGGCCT	CAGGGGCTTC	AGGGAGCCAG	CCTTCACCTA	10260
TGAGTCACCA	GACACTCGGG	GGTGGCCCCG	CCTTCAGGGT	GCTCACAGTC	TTCCCATCGT	10320
CCTGATCAA	GAGCAAGACC	AATGACTTCT	TAGGAGCAAG	CAGACACCCA	CAGGACACTG	10380
AGGTTCACCA	GAGCTGAGCT	GTCCTTTGA	ACCTAAAGAC	ACACAGCTCT	CGAAGGTTT	10440

CTCTTTAATC TGGATTAAG GCCTACTTGC CCCTCAAGAG GGAAGACAGT CCTGCATGTC	10500
CCCAGGACAG CCACTCGGTG GCATCCGAGG CCACTTAGTA TTATCTGACC GCACCTGGA	10560
ATTAATCGGT CCAAACGTGA CAAAAACCTT GGTGGGAAGT TTCATCCAG AGGCCTCAAC	10620
CATCCTGCTT TGACCAACCT GCATCTTTTT TTCTTTATG TGTATGCATG TATAATATA	10680
TATATATTTT TTTTTTTTC ATTTTTGGC TGCGCTGGCT GTTCGTTGCA GTTCGGTGCG	10740
CAGGCTTCTC TCTAGTTCT CTCTAGTCTT CTCTTATCAC AGAGCAGTCT CTAGACGATC	10800
GACGCGT	10807

(2) INFORMATION FOR SEQ ID NO:6:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATTCCGATC GACGCGTCGA CGATATACTC TAGACGATCG ACGCGTA 47

(2) INFORMATION FOR SEQ ID NO:7:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTACGCG TCGATCGTCT AGAGTATATC GTGACGCGT CGATCGG 47

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGGATCCCCT GCCGGTGCCCT CTGG

24

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AACGCGTCAT CCTCTGTGAG CCAG

24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) IMMEDIATE SOURCE:

(B) CLONE: ZC6839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACTACGTAGT

10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGTCACCTGA GAAGAAAACG AGACA

25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC6303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATTTGCGGCC GCCTGCAGCC ATGTGGCAGC TCACAAGCCT CCTGC

45

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC6337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAGGAAGGAG TTGGCGCGCT TGGGCCGTTG CAGCACCTGG TGGC

45

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC6306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTCTTCCTG AATTCTGTTT CTTGC

25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) IMMEDIATE SOURCE:

(B) CLONE: ZC6338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGATCCGCA AGCGCGCCAA CTCCCTCC

28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC6373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAAGTAAAAA AAGATCTAAA AATTAAC

28

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC6305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGTCTCGTT TTCTTCTTAA GTGACTGCGC TT

32

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC6302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTAAGAAGAA AACGAGACAC AGAAGACCAA GAAGACCAAG TAGATCCG

49

(2) INFORMATION FOR SEQ ID NO:19:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC6304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCTACTT GGTCTCTTG GTCTTCTGTG TCTCGTTTC TTC

43

(2) INFORMATION FOR SEQ ID NO:20:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Arg Lys Arg
1

(2) INFORMATION FOR SEQ ID NO:21:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Lys Arg Lys Arg
1

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser His Leu Arg Arg Lys Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACGCGTCGAC	CTGCAGGTCA	ACGGATCTCT	GTGTCTGTTT	TCATGTTAGT	ACACACGTG	60
TTTGGTGGCT	GTAGCTTCA	GCTACAGTCT	GAAGTCATAA	AGCCTGGTAC	CTCCAGCTCT	120
GTTCTCTCTC	AAGATTGTGT	TCTGCTGTTT	GGGTCTTAG	TGTCTCCACA	CAATTCTAG	180
AATTGTTTGT	TCTAGTTCTG	TGAAAAATGA	TGCTGGTATT	TTGATAAGGA	TTGCA"TGAA	240
TCTGTAAAGC	TACAGATATA	GTCATTGGGT	AGTACAGTCA	CTTAAACAAT	ATTAACCTCTT	300
CACATCTGTG	AGCATGATAT	ATTTTCCCCC	TCTATATCAT	CTTCAATTCC	TCCTA"CACT	360
TTCTTTCACT	GCAGTTTCT	GAGTACAGGT	CTTACACCTC	CTTGGTTAGA	GTCAT"CTTC	420
AGTATTTTAT	TCCTTGATA	CAATTGTGAA	TGAGGTAATT	TTCTTAGTTT	CTCTT"CTGA	480
TAGCTCATTG	TTAGTGTATA	TATAGAAAAG	CAACAGATTT	CTATGTATTA	ATTTTGTATC	540

CTGCAACAGA TTTCTATGTA TTAATTTGT ATCCTGCTAC TTTACGGAAT TCACTTATTA	600
GCTTTTGGT GACATCTTGA GGATTTCTG AAGAAAATGG CATGGTATGG TAGGACAAGG	660
TGTCATGTCA TCTGCAAACA GTGGCAGTTT TCCTTCTTCC CTTCCAACCT GGATTTCTT	720
GATTTCTTC TGCTGAGTA CGACTAGGAT TCCCAACT ATACCGAATA AAAGTGGCAA	780
GAGTGGACAT CCTTGTCTTA TTTTCTGAC CTTAGAGGAA ATGCTTCAG TTTTCACCA	840
TTAATTATAA TGTTTACTGT GGGCTTGTCATATGAGGTCTATT	900
CCCTCTATAC CCACCTTGTT GAGAGTTTT ATCATAAAAG TATGTTGAAT TTTGTCAAAA	960
GTTTTCTG CATCTATIGA GATGATTTT ACTCTTCAAT TCATTAATGA TTTTTATTCT	1020
TCATTTGTT AATGATTTC ATTCTTCAAT TTGTTAACGT GGTATATCAC ATTGATTGAT	1080
TTGTGGATAC CTTGTATCC CTGGGATAAA CCTCACTTGA TCATGAGCTT TCAATGTATT	1140
TTTGAATTCA CTTTGCTAAT ATTCTGTTGG GTATTTTGC ATCTCTATTCAATGATA	1200
TTGGCCTAAG AAAGGTTTG TCTGGTTTA GTATCAGGGT GATGCTGGCC TCATAGAGAG	1260
AGTTTACAAG CATTTCCTCC TCTTGATTT TTGGAATAG TTTGAGTAGG ATAGGTATTA	1320
ACTCTTCTT AAATGTTTG GGACTTCCCT GGTGAGCCGG TGTTGAGAA TCCGCCTCAG	1380
GGATGTGGGT TTGATCCCTG GTCAGGGAAC CATTAAAG ATCCCACATG CTGCAGGCAA	1440
CAAGCCCCCA AGCTGCAACC ACTGAGCTGC AACCGCTGCA GTGCCACAG GCCACGACCA	1500
GAGAAAGCCC ACATACAGCA GGGAAAGACCC AGCACAAACCG GAAAAAGGAG TTTGGTGGAA	1560
TACAGCTGTG AAGCCGTCTG GTCCTGGACT CCTGCTTGAG GGAATTTTT AAAAATTATI	1620
GATTCAATTTCATTACTGGT AACTGGTCTG TTCAATTTCCTTCTTCAGT	1680
CTTGGGAGAT TGTACATGCC TAGGAATGTG TCCGTTCTTCTAGTTGTCATTTATTG	1740
GACATGCATG GGAGCACACA GCACCGACCA GCGAGACTCA TGCTGGCTTC CTGGGGCCAG	1800
GCTGGGGCCC CAAGCAGCAT GGCATCCTAG AGTGTGTGAA AGCCCACGTGACCTGCCCCAG	1860
CCCCACAAATT TCATTCTGAG AAGTGATTCC TTGCTTCTGC ACTTACAGGC CCAGGATCTG	1920

ACCTGCTTCT	GAGGAGCAGG	GGTTTGGCA	GGACGGGAG	ATGCTGAGAG	CCGA	GGGGG	1980
TCCAGGTCCC	CTCCCAGGCC	CCCCTGTCTG	GGGCAGCCCT	TGGGAAAGAT	TGCC	CCAGTC	2040
TCCCTCCTAC	AGTGGTCAGT	CCCAGCTGCC	CCAGGCCAGA	GCTGCTTAT	TTCC	GTCTCT	2100
CTCTCTGGAT	GGTATTCTCT	GGAAGCTGAA	GGTTCTGAA	GTTATGAATA	GCTT	TGCCCT	2160
GAAGGGCATG	GTTTGTGGTC	ACGGTTACAA	GGAACTTGGG	AGACCCCTGCA	GCTCAGACGT		2220
CCCGAGATTG	GTGGCACCCA	GATTCCTAA	GCTCGCTGGG	GAACAGGGCG	CTTG	TTCTC	2280
CCTGGCTGAC	CTCCCTCCTC	CCTGCATCAC	CCAGTTCTGA	AAGCAGACCG	GTGCT	GGGGT	2340
CACAGCCTCT	CGCATCTAAC	GCCGGTGTCC	AAACCACCCG	TGCTGGTGT	CGGG	CGGCTA	2400
CCTATGGGGA	AGGGCTTCTC	ACTGCAGTGG	TGCCCCCGT	CCCTCTGAG	ATCAGAAGTC		2460
CCAGTCCCGA	CGTCAAACAG	GCCGAGCTCC	CTCCAGAGGC	TCCAGGGAGG	GATCC	TTGCC	2520
CCCCCGCTGC	TGCCTCCAGC	TCTGGTGCC	GCACCCCTG	GCCTGATCTT	GTAGA	CGCCT	2580
CAGTCTAGTC	TCTGCCTCCG	TGTTCACACG	CCCTCTCCCC	ATGTCCCCTC	CGTG	CCCCG	2640
TTTCTCTCA	CAAGGACACC	GGACATTAGA	TTAGCCCCTG	TTCCAGCCTC	ACCT	EAACAG	2700
CTCACATCTG	TAAAGACCTA	GATTCCAAAC	AAGATTCCAA	CCTGAAGTTC	CCGGT	GGATG	2760
TGAGTTCTGG	GGCGACATCC	TTCAACCCCA	TCACAGCTTG	CAGTTCATCG	CAAAC	CATGG	2820
AACCTGGGGT	TTATCGTAAA	ACCCAGGTTC	TTCATGAAAC	ACTGAGCTTC	GAGGCT	TGTT	2880
GCAAGAATT	AAGGTGCTAA	TACAGATCAG	GGCAAGGACT	GAAGCTGGCT	AAGC	CTCCTC	2940
TTTCCATCAC	AGGAAAGGGG	GGCCTGGGGG	CGGCTGGAGG	TCTGCTCCCC	TGAGT	GAGCT	3000
CTTCTCTGCT	ACAGTCACCA	ACAGTCTCTC	TGGGAAGGAA	ACCAGAGGCC	AGAGAGCAAG		3060
CCGGAGCTAG	TTAGGAGAC	CCCTGAACCT	CCACCCAAGA	TGCTGACCAG	CCAGC	3GGGCC	3120
CCCTGGAAAG	ACCCCTACAGT	TCAGGGGGGA	AGAGGGGCTG	ACCCGCCAGG	TCCCTGCTAT		3180
CAGGAGACAT	CCCCGCTATC	AGGAGATTCC	CCCACCTTGC	TCCCGTTCCC	CTAT	CCAAAT	3240

ACGCCACCC CACCCCTGTG ATGAGCAGTT TAGTCACCTTA GAATGTCAAC TGAAGGCTTT	3300
TGCATCCCT TTGCCAGAGG CACAAGGCAC CCACAGCCTG CTGGGTACCG ACGCCCATGT	3360
GGATTCAGCC AGGAGGCCTG TCCCTGCACCC TCCCTGCTCG GGCCCCCTCT GTGCTCAGCA	3420
ACACACCCAG CACCAGCATT CCCGCTGCTC CTGAGGTCTG CAGGCAGCTC GCTGTAGCCT	3480
GAGCGGTGTG GAGGAAGTG TCCTGGGAGA TTTAAATGT GAGAGGCGGG AGGTGGGAGG	3540
TTGGGCCCTG TGGGCCTGCC CATCCCACGT GCCTGCATTA GCCCCAGTGC TGCTCAGCCG	3600
TGCCCCCGCC GCAGGGTCA GGTCACTTTC CCGTCCTGGG GTTATTATGA CTCTTGTAT	3660
TGCCATTGCC ATTTTGCTA CCCTAACTGG GCAGCAGGTG CTTGCAGAGC CCTCGATACC	3720
GACCAGGTCC TCCCTCGGAG CTCGACCTGA ACCCCATGTC ACCCTTGCCC CAGCCTGCAG	3780
AGGGTGGGTG ACTGCAGAGA TCCCTTCACC CAAGGCCACG GTCACATGGT TTGGAGGAGC	3840
TGGTGCCCAA GGCAAGAGGCC ACCCTCCAGG ACACACCTGT CCCCCAGTGC GGCTCTGACC	3900
TGTCTTGTC TAAGAGGCTG ACCCCGGAAG TGTTCTGGC ACTGGCAGCC AGCCTGGACC	3960
CAGAGTCCAG ACACCCACCT GTGCCCGCGC TTCTGGGTG TACCAAGGAAC CGTCTAGGCC	4020
CAGAGGGGAC TTCTGCTTG GCCTTGGATG GAAGAAGGCC TCCTATTGTC CTCGTAGAGG	4080
AAGCCACCCC GGGGCCTGAG GATGAGCCAA GTGGGATTCC GGGAACCGCG TGCTGGGGG	4140
CCCAGCCCGG GCTGGCTGGC CTGCATGCCT CCTGTATAAG GCCCCAAGCC TGCTGTCTCA	4200
GCCCTCCACT CCCTGCAGAG CTCAGAAGCA CGACCCAGG GATATCATCG ATAAGCTTGG	4260
ATCCCCTGCC GGTGCCTCTG GGGTAAGCTG CCTGCCCTGC CCCACGTCTC GGGCACACAC	4320
ATGGGGTAGG GGGTCTTGGT GGGGCCTGGG ACCCCACATC AGGCCCTGGG GTCCCCCTG	4380
TGAGAAATGGC TGGAGCTGG GGTCCCTCCT GGCGACTGCA GAGCTGGCTG GCCGCGTGCC	4440
ACTCTTGTGG GTGACCTGTG TCCTGGCCTC ACACACTGAC CTCCCTCCAGC TCCTTCCAGC	4500
AGAGCTAAGG CTAAGTGAGC CAGAATGGTA CCTAAGGGGA GGCTAGCGGT CCTTCTCCCG	4560
AGGAGGGGCT GTCTGGAAC CACCAGCCAT GGAGAGGCTG GCAAGGGTCT GGCAGGTGCC	4620

CCAGGAATCA CAGGGGGGCC CCATGTCCAT T1CAGGGCCC GGGAGCCTTG GACTCCTCTG	4680
GGGACAGACG ACGTCACCAAC CGCCCCCCCC CCATCAGGGG GACTAGAAGG GACCAAGGACT	4740
GCAGTCACCC TTCCCTGGAC CCAGGCCCCCT CCAGGCCCCCT CCTGGGGCTC CTGCTCTGGG	4800
CAGCTTCTCC TTCAACCAATA AAGGCATAAA CCTGTGCTCT CCCTTCTGAG TCTTIGCTGG	4860
ACGACGGGCA GGGGGTGGAG AAGTGGTGGG GAGGGAGTCT GCCTCAGAGG ATGACAGCGG	4920
GGCTGGGATC CAGGGCGTCT GCATCACAGT CTTGTGACAA CTGGGGGCC ACACACATCA	4980
CTGCGGCTCT TTGAAACTTT CAGGAACCAAG GGAGGGACTC GGCAAGAGACA TCTGCGAGTT	5040
CACTTGGAGT GTTCAGTCAA CACCCAAACT CGACAAAGGA CAGAAAGTGG AAAA"GGCTG	5100
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ATGATCCAGC CAGCCACTAC TGTCGTATCA ACTCATGTAC CCAAACGCAC TGATCTGTCT	5220
GGCTAATGAT GAGAGATTCC CAGTAGAGAG CTGGCAAGAG GTCACAGTGA GAACTGTCTG	5280
CACACACAGC AGAGTCCACC AGTCATCCTA AGGAGATCAAG TCCTGGTGTT CATTGGAGGA	5340
CTGATGTTGA AGCTGAAACT CCAATGCTTT GGCCACCTGA TGTGAAGAGC TGACTCATTT	5400
GAAAAGACCC TGATGCTGGG AAAGATTGAG GGCAGGAGGA GAAGGGGACG ACAGAGGATG	5460
AGATGGTTGG ATGGCATCAC CAACACAATG GACATGGTT TGTTGGACT CCAGGAGTTG	5520
GTGATGGACA GGGAGGCCTG GCGTGCTACG GAAGGGTTT ATGGGGTCAC AAAGACTGAG	5580
TGACTGAACG GAGCTGAACG GAATGGAAT GAGGTATACA GCAAAGTGGG GATTTTTAG	5640
ATAATAAGAA TATACACATA ACATAGTGTAA TACTCATATT TTTATGCATA CCTGATGCT	5700
CAGTCACTCA GTCGTATCTG ACTCTGTGAC CTATGGACCG TAGCCTTCCA GGTTTCTTCT	5760
GTCCACAGAA TTCTCCAAGG CAAGAATACT GGAGTGGTA GCCATTTCT CCTCCAGGGG	5820
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CTGTGCCACC AGAGAAGCCC GTGTTACTCT CTATGTCCCC CTTAATTACCA AAAGCTGCTC	5940

CAAGAAAAAG CCCCTGTGCC CTCTGAGCTT CCCGGCCTGC AGAGGGTGGT GGGGGTAGAC	6000
TGTGACCTGG GAACACCCCTC CCGCTTCAGG ACTCCCCGGC CACGTGACCC ACAGTCCTGC	6060
AGACAGCCGG GTAGCTCTGC TCTTCAGGC TCATTATCTT TAAAAAAAAC TGAGGTCTAT	6120
TTTGTGACTT CGCTGCCGTA ACTTCTGAAC ATCCAGTGCG ATGGACAGGA CCTCCTCCCC	6180
AGGCCTCAGG GGCTTCAGGG AGCCAGCCTT CACCTATGAG TCACCAGACA CTCGGGGGTG	6240
GCCCCGCCTT CAGGGTGCCTC ACAGTCTTCC CATGTCCTG ATCAAAGAGC AAGACCAATG	6300
ACTTCTTAGG AGCAAGCAGA CACCCACAGG ACACTGAGGT TCACCAGAGC TGAGCTGTCC	6360
TTTTGAACCT AAAGACACAC AGCTCTCGAA GGTTTTCTCT TTAATCTGGA TTAAAGGCCT	6420
ACTTGGCCCT CAAGAGGGAA GACAGTCCTG CATGTCCCCA GGACAGCCAC TCGGTGGCAT	6480
CCGAGGCCAC TTAGTATTAT CTGACCGCAC CCTGGAATTAA ATCGGTCAA ACTGGACAAA	6540
AACCTTGGTG GGAAGTTCA TCCCAGAGGC CTCAACCATC CTGCTTGAC CACCCCTGCAT	6600
CTTTTTTTCT TTATGTGTA TGCATGTATA TATATATATA TATTTTTTTT TTTTCATT	6660
TTTGGCTGTG CTGGCTGTTG GTTGCAGTTG GGTGCGCAGG CTTCTCTCTA GTTTCTCTCT	6720
AGTCTCTCT TATCACAGAG CAGTCTCTAG ACGATCGACG CGT	6763

(2) INFORMATION FOR SEQ ID NO:24:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Arg	Ile	Arg	Lys	Arg
1				5

(2) INFORMATION FOR SEQ ID NO:25:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln Arg Arg Lys Arg
1 5

CLAIMS

1. A method for producing protein C in a transgenic animal comprising:

providing a DNA construct comprising a first DNA segment encoding a secretion signal and a protein C propeptide operably linked to a second DNA segment encoding protein C, wherein the encoded protein C comprises a two-chain cleavage site modified from Lysine (Lys)-Arginine (Arg) to R₁-R₂-R₃-R₄, and wherein each of R₁, R₂, R₃, R₄ is individually Lys or Arg, and wherein said first and second segments are operably linked to additional DNA segments required for expression of the protein C DNA in a mammary gland of a host female animal;

introducing said DNA construct into a fertilized egg of a non-human mammalian species;

inserting said egg into an oviduct or uterus of a female of said species to obtain offspring carrying said DNA construct;

breeding said offspring to produce female progeny that express said first and second DNA segments and produce milk containing protein C encoded by said second segment, wherein said protein has anticoagulant activity upon activation;

collecting milk from said female progeny; and recovering the protein C from the milk.

2. The method of claim 1, further comprising the step of activating the protein C.

3. The method of claim 1, wherein R₁-R₂-R₃-R₄ is Arg-Arg-Lys-Arg (SEQ ID NO: 20).

4. The method of claim 1, wherein said species is selected from sheep, rabbits, cattle and goats.

5. The method of claim 1, wherein each of said first and second DNA segments comprises an intron.

6. The method of claim 1, wherein the second DNA segment comprises a DNA sequence of nucleotides as shown in Seq. ID NO: 1 or Seq. ID. NO: 3.

7. The method of claim 6, wherein the second DNA segment comprises the DNA sequence of nucleotides as shown in SEQ. ID. NO: 1.

8. The method of claim 1, wherein the additional DNA segments comprise a transcriptional promoter selected from the group consisting of casein, β -lactoglobulin, α -lactalbumin and whey acidic protein gene promoters.

9. The method of claim 8, wherein the transcriptional promoter is the β -lactoglobulin gene promoter.

10. A transgenic non-human female mammal that produces recoverable amounts of human protein C in its milk, wherein at least 90% of the human protein C in the milk is two-chain protein C.

11. A process for producing a transgenic offspring of a mammal comprising:

providing a DNA construct comprising a first DNA segment encoding a secretion signal and a protein C propeptide operably linked to a second DNA segment encoding protein C, wherein the encoded protein C comprises a two-chain cleavage site modified from Lys-Arg to R₁-R₂-R₃-R₄, and wherein each of R₁, R₂, R₃, R₄, is individually Lys or Arg, and wherein said first and second segments are operably linked to additional DNA segments required for expression of the protein C DNA in the mammary gland of a host female animal;

introducing said DNA construct into a fertilized egg of a non-human mammalian species; and

inserting said egg into an oviduct or uterus of a female of said species to obtain offspring carrying said DNA construct.

12. The process according to claim 11, wherein R₁-R₂-R₃-R₄ is Arg-Arg-Lys-Arg (SEQ ID NO: 20).

13. The process according to claim 11, wherein the offspring is female.

14. The process according to claim 11, wherein the offspring is male.

15. A non-human mammal produced according to the process of claim 10.

16. A non-human mammal of claim 15, wherein the mammal is female.

17. A female mammal according to claim 16 that produces milk containing protein C encoded by said DNA construct, wherein said protein C has anticoagulant activity upon activation.

18. A non-human mammalian embryo containing in its nucleus a heterologous DNA segment encoding protein C, wherein the encoded protein C comprises a two-chain cleavage site modified from Lys-Arg to R₁-R₂-R₃-R₄, and wherein each of R₁, R₂, R₃, R₄, is individually Lys or Arg.

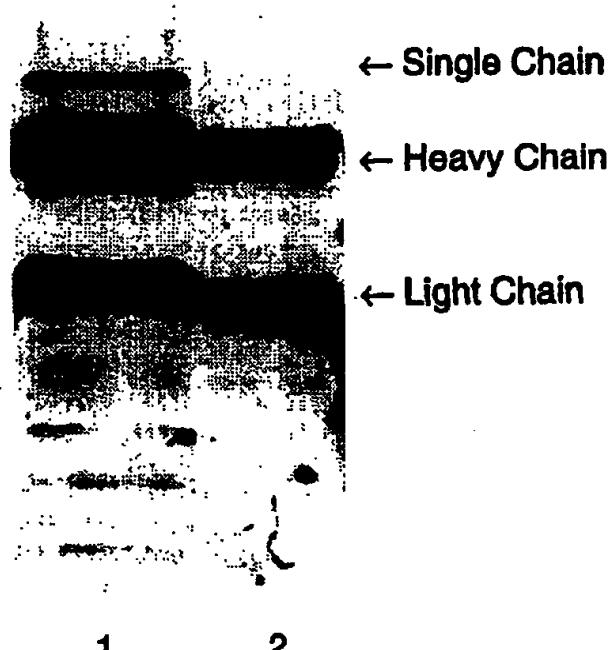


Fig. 1

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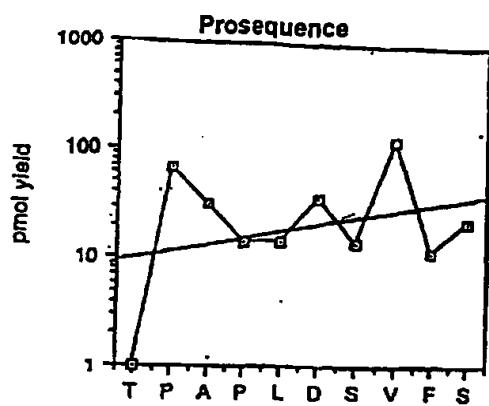


Fig. 2a

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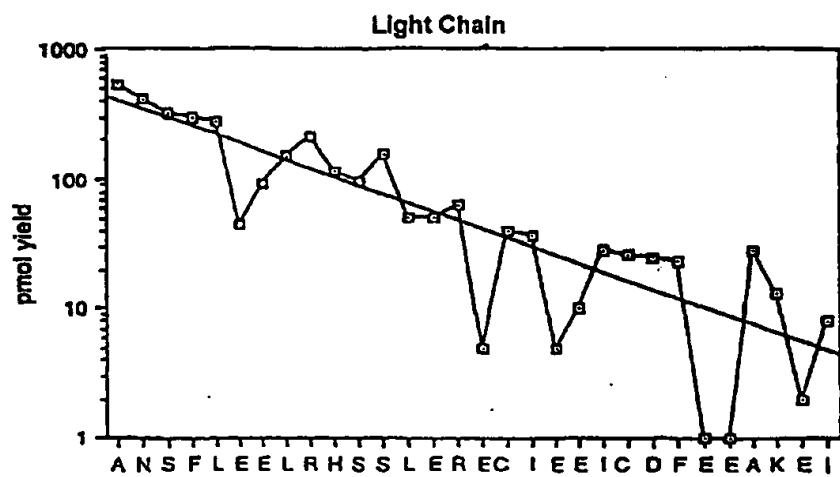


Fig. 2b

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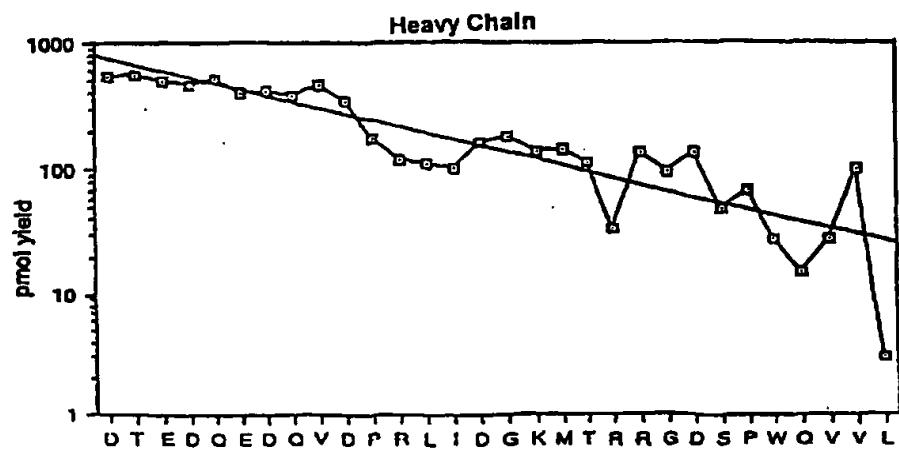


Fig. 2c

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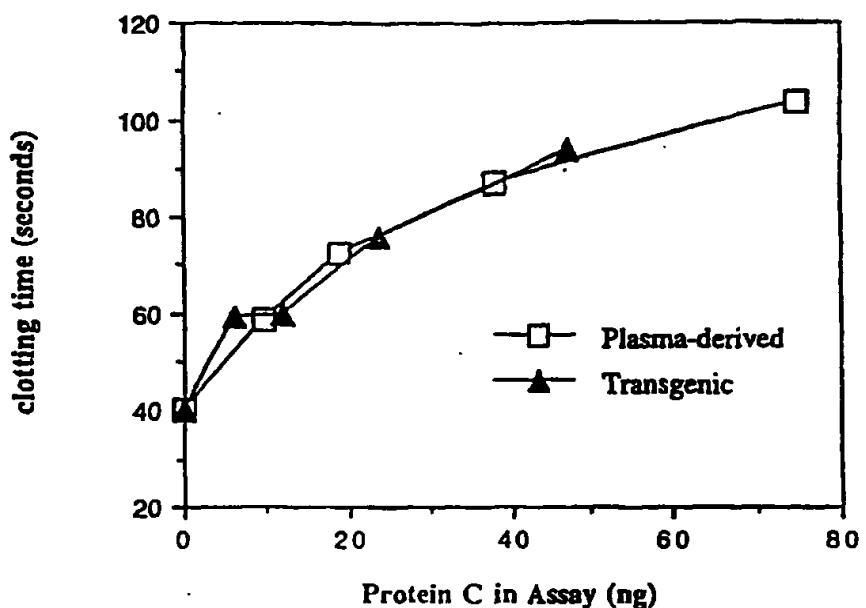


Fig. 3

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INTERNATIONAL SEARCH REPORT

In World Application No
PCT/US 96/18866

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/00 C12N9/64 A01K67/027

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N A01K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>TRANSGENIC RESEARCH, vol. 3, 1994, pages 355-364, XP000647718</p> <p>W. DROHAN ET AL: "Inefficient processing of human protein C in the mouse mammary gland" cited in the application see the whole document especially page 362, right column, lines 11-19</p> <p>---</p> <p>-/-</p>	1-18

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents:

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- *E* earlier document but published on or after the international filing date
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- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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Date of the actual completion of the international search

25 March 1997

Date of mailing of the international search report

02.04.97

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Authorized officer

Van der Schaaf, C

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International Application No.
PCT/US 96/18866

C(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Character of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MIAMI BIO/TECHNOLOGY WINTER SYMPOSIUM ON ADVANCES IN GENE TECHNOLOGY: PROTEIN ENGINEERING AND STRUCTURAL BIOLOGY, MIAMI, FLORIDA, USA, FEBRUARY 4-9, 1995. PROTEIN ENGINEERING 8 (SUPPL.). 1995. 107. ISSN: 0269-2139, XP002028254 COLMAN A ET AL: "The transgenic mammary gland as a bioreactor: Expectations and realisations." see page 107, left-hand column, paragraph 5 last lines ---	1-18
Y	BIOCHEMISTRY, vol. 29, 1990, pages 347-354, XP002028255 D. FOSTER ET AL: "Endoproteolytic processing of the dibasic cleavage site in the human protein C precursor in transfected mammalia cells: Effects of sequence alterations on efficiency of cleavage" see the whole document ---	1-18
Y	EP 0 319 312 A (LILLY CO ELI) 7 June 1989 see the whole document ---	1-18
Y	WO 88 00239 A (PHARMACEUTICAL PROTEINS LTD) 14 January 1988 cited in the application see the whole document ---	4,8,9
Y	WO 92 11757 A (AMERICAN NAT RED CROSS) 23 July 1992 see the whole document especially page 11 and 12 ---	1-18
P,A	WO 96 34966 A (AMERICAN NAT RED CROSS) 7 November 1996 -----	
2		

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INTERNATIONAL SEARCH REPORT

Information on patent family members

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PCT/US 96/18866

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